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OM protein - protein search, using sw model

Run on: May 11, 2006, 11:29:52 ; Search time 184 Seconds
(without alignments)
47.759 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREBEKPF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	20	ADS13770	Ads13770 Human Ang
2	106	100.0	20	ADS13769	Ads13769 Human Ang
3	106	100.0	26	ADS13805	Ads13805 Ang-1 lin
4	106	100.0	235	AAE32344	AAE32344 Human ang
5	106	100.0	261	ADI23636	ADI23636 Human Ang
6	106	100.0	298	ADI23638	ADI23638 Yeast GCN
7	106	100.0	310	ADI23640	ADI23640 Human CMP
8	106	100.0	312	ADI23642	ADI23642 Human COM
9	106	100.0	402	7 AAE38503	AAE38503 Human ang
10	106	100.0	402	9 AEA81248	AEA81248 Human ang
11	106	100.0	456	8 ADS13776	ADS13776 Mouse Ang
12	106	100.0	456	8 ADS13775	ADS13775 Human Ang
13	106	100.0	494	2 AAW47526	AAW47526 Amino aci
14	106	100.0	498	2 AAR94603	AAR94603 Human TIE
15	106	100.0	498	2 AAW01409	AAW01409 Human TIE
16	106	100.0	498	2 AAW47530	AAW47530 Amino aci
17	106	100.0	498	2 AAW47528	AAW47528 Amino aci
18	106	100.0	498	3 AAY78905	AAY78905 Human ang
19	106	100.0	498	3 AAY78902	AAY78902 Human ang
20	106	100.0	498	3 AAB28391	AAB28391 Human ang
21	106	100.0	498	5 AAU77943	AAU77943 Amino aci
22	106	100.0	498	6 ABP58063	ABP58063 Human ang
23	106	100.0	498	6 AAE32342	AAE32342 Human ang
24	106	100.0	498	7 AAE38487	AAE38487 Human ang

25	106	100.0	498	7 AAE38507	AAE38507 Human ang
26	106	100.0	498	7 AAE38501	AAE38501 Human ang
27	106	100.0	498	7 AAE38499	AAE38499 Mouse ang
28	106	100.0	498	7 AAE38486	AAE38486 Human ang
29	106	100.0	498	7 AAE38497	AAE38497 Mouse ang
30	106	100.0	498	7 ADD69265	ADD69265 Human ang
31	106	100.0	498	7 ADF72296	ADF72296 Human ang
32	106	100.0	498	8 ADQ19778	ADQ19778 Human sof
33	106	100.0	498	8 ADR87238	ADR87238 Amino aci
34	106	100.0	498	8 ADS13782	ADS13782 Mouse ang
35	106	100.0	498	8 ADS13781	ADS13781 Human ang
36	106	100.0	498	8 ADZ80187	ADZ80187 Human TIE
37	106	100.0	498	9 AEA81247	AEA81247 Human ang
38	106	100.0	498	9 AEB87759	AEB87759 Human Ang
39	96	90.6	495	3 AAY78907	AAY78907 Angiopoie
40	96	90.6	495	3 AAY78904	AAY78904 Angiopoie
41	96	90.6	495	3 AAB28393	AAB28393 Human ang
42	96	90.6	495	5 AAU77945	AAU77945 Amino aci
43	96	90.6	498	7 AAE38493	AAE38493 Pig angio
44	93	87.7	27	8 ADS13806	ADS13806 Ang-1 lin
45	89.5	84.4	147	7 AAE38508	AAE38508 Human ang

ALIGNMENTS

RESULT 1
ADS13770
ID ADS13770 standard; peptide; 20 AA.
XX
AC ADS13770;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human Ang-1 protein ECM-binding fragment.
XX
XX Ang-1; extracellular matrix; ECM; angiotensin; vasotrophic;
XX anti-diabetic; antiarthritic; cerebroprotective; antiangiogenic;
XX gene therapy; human.
XX
XX Homo sapiens.
XX
XX W02004076650-A2.
XX
XX 10-SEP-2004.
XX
XX 27-FEB-2004; 2004WO-US006101.
XX
XX 27-FEB-2003; 2003US-0450582P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Yu Q;
XX
XX WPI; 2004-653413/63.
XX
XX N-PSDB; ADS13788.
XX
XX New pharmaceutical composition comprises a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or ischemia.
XX
XX Claim 1; SEQ ID NO 2; 114pp; English.
XX
XX The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patients with the diseases

CC related to lack of blood vessels such as ischaemia in hearts and limbs;
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
 CC atherosclerosis risk by maintaining the health and integrity of blood
 CC vessels; to assist the recovery of the patients who had stroke and the
 CC angioplasty procedure by promoting the growth/survival of endothelial
 CC cells and establish endothelial monolayer and inhibit excessive
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;
 CC to treat patients with restenosis by inhibiting re-closure of blood
 CC vessel after inserting stents into blood vessels; to make stable and
 CC functional artificial blood vessels comprising using the composition
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;
 CC of treating an individual suspected of having cancer; of preventing
 CC diabetes and/or arthritis in an individual suspected of being at risk of
 CC developing diabetes or arthritis. The pharmaceutical composition is
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
 CC angiogenesis, or arthritis. The present sequence represents an ECM-
 CC binding fragment of Ang-1 protein.

XX Sequence 20 AA;

Query Match 100.0%; Score 106; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.9e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20
 |||||
 Db 1 LCTKEGVLKGGKREKEKPF 20

RESULT 2

ADSL3769

ID ADSL3769 standard; peptide; 20 AA.

AC ADSL3769;
 DT 02-DEC-2004 (first entry)
 DE Human Ang-1 protein ECM-binding fragment.

XX Ang-1; extracellular matrix; ECM; angiotensin; cytostatic; vasotropic;
 KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;
 KW gene therapy; human.

XX Homo sapiens.

XX WO2004076650-A2.

XX 10-SEP-2004.

XX 27-FEB-2004; 2004WO-US006101.

XX 27-FEB-2003; 2003US-0450582P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Yu Q;

XX WPI; 2004-653413/63.

XX N-PSDB; ADSL3787.

XX New pharmaceutical composition comprises a pharmaceutical carrier and an
 PT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein
 PT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
 PT ischemia.

PS Claim 1; SEQ ID NO 1; 114pp; English.

XX The invention relates to a pharmaceutical composition comprising a
 CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-
 CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also
 CC provided are methods of treating an individual suspected of having
 CC coronary artery disease, vascular disease or a condition involving

CC ischaemia; of promoting angiogenesis, endothelial survival and
 CC maintaining vascular integrity in an individual; of treating an
 CC individual suspected of having a disease related to lack of blood vessels
 CC to effectively promote angiogenesis in the patients with the diseases
 CC related to lack of blood vessels such as ischaemia in hearts and limbs;
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
 CC atherosclerosis risk by maintaining the health and integrity of blood
 CC vessels; to assist the recovery of the patients who had stroke and the
 CC angioplasty procedure by promoting the growth/survival of endothelial
 CC cells and establish endothelial monolayer and inhibit excessive
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;
 CC to treat patients with restenosis by inhibiting re-closure of blood
 CC vessel after inserting stents into blood vessels; to make stable and
 CC functional artificial blood vessels comprising using the composition
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;
 CC of treating an individual suspected of having cancer; of preventing
 CC diabetes and/or arthritis in an individual suspected of being at risk of
 CC developing diabetes or arthritis. The pharmaceutical composition is
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
 CC angiogenesis, or arthritis. The present sequence represents an ECM-
 CC binding fragment of Ang-1 protein.

XX Sequence 20 AA;

Query Match 100.0%; Score 106; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.9e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20
 |||||
 Db 1 LCTKEGVLKGGKREKEKPF 20

RESULT 3

ADSL3805

ID ADSL3805 standard; peptide; 26 AA.

XX ADSL3805;

XX 02-DEC-2004 (first entry)

XX Ang-1 linker peptide region.

XX Ang-1; extracellular matrix; ECM; angiotensin; cytostatic; vasotropic;
 KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;
 KW gene therapy.

XX Homo sapiens.

XX WO2004076650-A2.

XX 10-SEP-2004.

XX 27-FEB-2004; 2004WO-US006101.

XX 27-FEB-2003; 2003US-0450582P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Yu Q;

XX WPI; 2004-653413/63.

XX New pharmaceutical composition comprises a pharmaceutical carrier and an
 PT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein
 PT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
 PT ischemia.

PS Example 1; Page 27; 114pp; English.

XX The invention relates to a pharmaceutical composition comprising a
 CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-

CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also
CC provided are methods of treating an individual suspected of having
CC coronary artery disease, vascular disease or a condition involving
CC ischaemia; of promoting angiogenesis, endothelial survival and
CC maintaining vascular integrity in an individual; of treating an
CC individual suspected of having a disease related to lack of blood vessels
CC to effectively promote angiogenesis in the patients with the diseases
CC related to lack of blood vessels such as ischaemia in hearts and limbs;
CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
CC atherosclerosis risk by maintaining the health and integrity of blood
CC vessels; to assist the recovery of the patients who had stroke and the
CC angioplasty procedure by promoting the growth/survival of endothelial
CC cells and establish endothelial monolayer and inhibit excessive
CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;
CC to treat patients with restenosis by inhibiting re-closure of blood
CC vessel after inserting stents into blood vessels; to make stable and
CC functional artificial blood vessels comprising using the composition
CC above; of identifying compounds that modulates binding of Ang-1 to ECM;
CC of treating an individual suspected of having cancer; of preventing
CC diabetes and/or arthritis in an individual suspected of being at risk of
CC developing diabetes or arthritis. The pharmaceutical composition is
CC useful for treating diseases and disorders, e.g. cancer, coronary artery
CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
CC angiogenesis, or arthritis. The present sequence represents a linker
CC peptide region of Ang-1 protein.

XX SQ Sequence 26 AA;

Query Match 100.0%; Score 106; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
| | | | | | | | | | | | | | | | | | | | | |
Db 7 LCTKEGVLKGGKREBEKPF 26

RESULT 4
AAE32344
ID AAE32344 standard; protein; 235 AA.

XX AC AAE32344;

XX DT 24-MAR-2003 (first entry)

XX DE Human angiotensin-1 (Ang-1) truncated protein #1.

XX KW Vascular endothelial growth factor; VEGF; angiogenesis; wound healing;
XX KW bone growth; osteoporosis; osteoarthritis; bone reconstruction; ulcer;
XX KW lesion; injury; trauma; periodontal condition; protein therapy; human;
XX KW angiotensin-1; Ang-1.

XX OS Homo sapiens.

XX FN WO200283851-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011406.

XX PR 10-APR-2001; 2001US-00832355.

XX PA (GENV-) GENVEC INC.

XX PI Kovesdi I, Kessler PD;

XX DR WPI; 2003-075536/07.

XX New fusion protein comprising a non-heparin-binding vascular endothelial
XX growth factor (VEGF) peptide portion and a non-VEGF peptide portion,
XX useful for promoting angiogenesis and/or bone growth in mammals.

XX Disclosure; Page 126-127; 191pp; English.

XX The invention relates to a fusion protein comprising non-heparin binding
CC vascular endothelial growth factor (VEGF) peptide portion and a non-VEGF
CC peptide portion useful for promoting angiogenesis and/or bone growth in
CC mammalian host. The fusion protein is useful for promoting angiogenesis,
CC wound healing and bone growth. Compositions containing bone growth
CC promoting fusion protein can be used to treat osteoporosis, rheumatoid or
CC osteoarthritis, to improve poor bone healing, to promote implant
CC integration and function of artificial joints and to facilitate bone
CC reconstruction. They can also be used to treat e.g. ulcers, lesions,
CC injuries, burns, trauma, periodontal conditions, lacerations and other
CC conditions. The invention is also useful in protein therapy. The present
CC sequence is human angiotensin-1 (Ang-1) truncated protein used in the
CC invention

XX SQ Sequence 235 AA;

Query Match 100.0%; Score 106; DB 6; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
| | | | | | | | | | | | | | | | | | | | | |
Db 215 LCTKEGVLKGGKREBEKPF 234

RESULT 5
ADI23636

ID ADI23636 standard; protein; 261 AA.

XX AC ADI23636;

XX DT 22-APR-2004 (first entry)

XX DE Human Ang-1 fibrinogen-like domain/Preprotrypsin signal.

XX KW Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;
XX KW angiotensin; coiled-coil domain; cell growth; proliferation;
XX KW matrix protein; transcription factor; growth factor; secretory protein;
XX KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;
XX KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;
XX KW endothelial precursor cell.

XX OS Homo sapiens.

XX Synthetic.

XX PN US2003220476-A1.

XX PD 27-NOV-2003.

XX PF 18-OCT-2002; 2002US-00273180.

XX PR 21-MAY-2002; 2002US-0382541P.

XX PA (KOHG/) KOH G Y.

XX PI Koh GY;

XX DR WPI; 2004-010899/01.

XX DR N-PSDB; ADI23635.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked
XX to either a receptor binding domain of ligand or ligand binding domain of
XX a receptor, useful for inhibiting or promoting differential function.

XX PS Disclosure; SEQ ID NO 2; 38pp; English.

XX The invention relates to a coiled coil chimaeric molecule comprising a
XX coiled-coil domain linked to either a receptor binding domain of a ligand
XX or ligand binding domain of a receptor, which forms a biologically active
XX multimer, and where the chimaeric molecule in its non-multimeric form is
XX not biologically active. Also included are an isolated nucleic acid
XX encoding the coiled coil chimaeric molecule, an expression vector

comprising the nucleic acid, a host cell comprising the vector, a soluble biologically active multimer comprising the coiled coil chimaeric molecule, promoting cell growth or proliferation, decreasing or inhibiting ligand activity or cell proliferation and making a chimaeric molecule. The coiled coil chimaeric molecule comprises a domain belonging to a matrix protein family, transcription factor family, growth factor family or secretory protein family. The coiled coil domain is from cartilage matrix protein (CMP) or cartilage oligomeric matrix protein (COMP). The receptor-binding domain binds to Tie2 or Tiel receptor. The receptor-binding domain is a fibrinogen-like domain of angiotensin-1, -2, -3 or -4. The chimaeric molecules are useful for promoting or inhibiting a differential function and/or influencing the phenotype of cells as growth, survival, contractility, migration and/or proliferation of receptor-bearing cells such as endothelial cells, haematopoietic stem cells and endothelial precursor cells. The present sequence represents the fibrinogen-like domain of Ang-1 with a preprotrypsin leader.

Sequence 261 AA;
 Query Match 100.0%; Score 106; DB 8; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.4e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREKEKPF 20
 |||||
 Db 139 LCTKEGVLLKGGKREKEKPF 158

RESULT 6
 ADI23638
 ID ADI23638 standard; protein; 298 AA.

XX AC ADI23638;

XX DT 22-APR-2004 (first entry)

XX DE Yeast GCN4 coiled-coil domain/Human Ang-1 cDNA.

XX KW Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal; angiotensin; coiled-coil domain; cell growth; proliferation; matrix protein; transcription factor; growth factor; secretory protein; cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP; Tie2 receptor; Tiel receptor; endothelial cell; haematopoietic stem cell; endothelial precursor cell; yeast.

XX OS Homo sapiens.
 OS Saccharomyces cerevisiae.
 OS Chimeric.

XX PN US2003220476-A1.

XX PD 27-NOV-2003.

XX PF 18-OCT-2002; 2002US-00273180.

XX PR 21-MAY-2002; 2002US-0382541P.

XX PA (KOHG/) KOH G Y.

XX PI Koh GY;

XX DR WPI; 2004-010889/01.

XX DR N-PSDB; ADI23637.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of ligand or ligand binding domain of a receptor, useful for inhibiting or promoting differential function.

XX Example 5; SEQ ID NO 4; 38pp; English.

XX The invention relates to a coiled coil chimaeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of a ligand or ligand binding domain of a receptor, which forms a biologically active

CC multimer, and where the chimaeric molecule in its non-multimeric form is not biologically active. Also included are an isolated nucleic acid encoding the coiled coil chimaeric molecule, an expression vector comprising the nucleic acid, a host cell comprising the vector, a soluble biologically active multimer comprising the coiled coil chimaeric molecule, promoting cell growth or proliferation, decreasing or inhibiting ligand activity or cell proliferation and making a chimaeric molecule. The coiled coil chimaeric molecule comprises a domain belonging to a matrix protein family, transcription factor family, growth factor family or secretory protein family. The coiled coil domain is from cartilage matrix protein (CMP) or cartilage oligomeric matrix protein (COMP). The receptor-binding domain binds to Tie2 or Tiel receptor. The receptor-binding domain is a fibrinogen-like domain of angiotensin-1, -2, -3 or -4. The chimaeric molecules are useful for promoting or inhibiting a differential function and/or influencing the phenotype of cells as growth, survival, contractility, migration and/or proliferation of receptor-bearing cells such as endothelial cells, haematopoietic stem cells and endothelial precursor cells. The present sequence represents the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-coil domain.

Sequence 298 AA;

Query Match 100.0%; Score 106; DB 8; Length 298;

Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREKEKPF 20
 |||||
 Db 64 LCTKEGVLLKGGKREKEKPF 83

RESULT 7

ADI23640

ID ADI23640 standard; protein; 310 AA.

XX AC ADI23640;

XX DT 22-APR-2004 (first entry)

XX DE Human CMP coiled-coil domain/Ang-1.

XX KW Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal; angiotensin; coiled-coil domain; cell growth; proliferation; matrix protein; transcription factor; growth factor; secretory protein; cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP; Tie2 receptor; Tiel receptor; endothelial cell; haematopoietic stem cell; endothelial precursor cell.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN US2003220476-A1.

XX PD 27-NOV-2003.

XX PF 18-OCT-2002; 2002US-00273180.

XX PR 21-MAY-2002; 2002US-0382541P.

XX PA (KOHG/) KOH G Y.

XX PI Koh GY;

XX DR WPI; 2004-010889/01.

XX DR N-PSDB; ADI23639.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of ligand or ligand binding domain of a receptor, useful for inhibiting or promoting differential function.

XX Example 6; SEQ ID NO 6; 38pp; English.

CC The invention relates to a coiled coil chimaeric molecule comprising a
 CC coiled-coil domain linked to either a receptor binding domain of a ligand
 CC or ligand binding domain of a receptor, which forms a biologically active
 CC multimer, and where the chimaeric molecule in its non-multimeric form is
 CC not biologically active. Also included are an isolated nucleic acid
 CC encoding the coiled coil chimaeric molecule, an expression vector
 CC comprising the nucleic acid, a host cell comprising the vector, a soluble
 CC biologically active multimer comprising the coiled coil chimaeric
 CC molecule, promoting cell growth or proliferation, decreasing or
 CC inhibiting ligand activity or cell proliferation and making a chimaeric
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging
 CC to a matrix protein family, transcription factor family, growth factor
 CC family or secretory protein family. The coiled coil domain is from
 CC cartilage matrix protein (CMP) or cartilage oligomeric matrix protein
 CC (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or
 CC inhibiting a differential function and/or influencing the phenotype of
 CC as growth, survival, contractility, migration and/or proliferation of
 CC receptor-bearing cells such as endothelial cells, haematopoietic stem
 CC cells and endothelial precursor cells. The present sequence represents
 CC the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-
 CC coil domain.
 XX
 SQ Sequence 310 AA;

Query Match 100.0%; Score 106; DB 8; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREBEKPF 20
 |||||
 Db 76 LCTKEGVLLKGGKREBEKPF 95

RESULT 8
 ADI23642
 ID ADI23642 standard; protein; 312 AA.
 XX
 AC ADI23642;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human COMP coiled-coil domain/Ang-1.

XX Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;
 KW angiotensin; coiled-coil domain; cell growth; proliferation;
 KW matrix protein; transcription factor; growth factor; secretory protein;
 KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;
 KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;
 KW endothelial precursor cell.

XX Homo sapiens.
 OS Synthetic.
 OS
 PN US2003220476-A1.

XX 27-NOV-2003.
 XX
 XX 18-OCT-2002; 2002US-00273180.
 XX
 XX 21-MAY-2002; 2002US-0382541P.

XX (KOHG/) KOH G Y.
 XX Koh GY;
 XX

XX WPI; 2004-010889/01.
 XX N-PSDB; ADI23641.
 XX

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked
 PT to either a receptor binding domain of ligand or ligand binding domain of
 PT a receptor, useful for inhibiting or promoting differential function.

XX Example 7; SEQ ID NO 8; 38pp; English.
 XX

CC The invention relates to a coiled coil chimaeric molecule comprising a
 CC coiled-coil domain linked to either a receptor binding domain of a ligand
 CC or ligand binding domain of a receptor, which forms a biologically active
 CC multimer, and where the chimaeric molecule in its non-multimeric form is
 CC not biologically active. Also included are an isolated nucleic acid
 CC encoding the coiled coil chimaeric molecule, an expression vector
 CC comprising the nucleic acid, a host cell comprising the vector, a soluble
 CC biologically active multimer comprising the coiled coil chimaeric
 CC molecule, promoting cell growth or proliferation, decreasing or
 CC inhibiting ligand activity or cell proliferation and making a chimaeric
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging
 CC to a matrix protein family, transcription factor family, growth factor
 CC family or secretory protein family. The coiled coil domain is from
 CC cartilage matrix protein (CMP) or cartilage oligomeric matrix protein
 CC (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or
 CC inhibiting a differential function and/or influencing the phenotype of
 CC as growth, survival, contractility, migration and/or proliferation of
 CC receptor-bearing cells such as endothelial cells, haematopoietic stem
 CC cells and endothelial precursor cells. The present sequence represents
 CC the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-
 CC coil domain.
 XX
 SQ Sequence 312 AA;

Query Match 100.0%; Score 106; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREBEKPF 20
 |||||
 Db 78 LCTKEGVLLKGGKREBEKPF 97

RESULT 9
 AAE38503
 ID AAE38503 standard; protein; 402 AA.
 XX
 AC AAE38503;

XX 20-NOV-2003 (first entry)
 XX Human angiotensin-1 #4.

XX Angiotensin-1; endothelium; cell proliferation; tumour; gene therapy;
 KW human.
 KW
 XX Homo sapiens.
 OS
 PN WO2003068165-A2.

XX 21-AUG-2003.
 XX
 XX 14-FEB-2003; 2003WO-US004595.

XX 14-FEB-2002; 2002US-0356809P.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Ellis LM;
 XX WPI; 2003-697465/66.

XX Stabilizing the endothelium or reducing endothelial cell proliferation
 PT associated with a tumor comprises administering to a patient having a
 PT tumor angiotensin-1 polypeptide.
 XX
 XX Disclosure; Page 139-140; 157pp; English.
 XX

CC The invention relates to a method for stabilising the endothelium or
 CC reducing endothelial cell proliferation associated with a tumour by
 CC administering angiotensin-1 polypeptide to a patient having tumour. The
 CC method is useful for stabilising the endothelium or reducing endothelial
 CC cell proliferation associated with a tumour. It is also useful in gene
 CC therapy. The present sequence is human angiotensin-1. This sequence is
 CC used to illustrate the method of the invention
 XX
 SQ Sequence 402 AA;

Query Match 100.0%; Score 106; DB 7; Length 402;
 Best Local Similarity 100.0%; Pred. No. 2.2e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLKGGKREBEKPF 20
 Db 264 LCTKEGVLKGGKREBEKPF 283

RESULT 10
 AEA81248
 ID AEA81248 standard; protein; 402 AA.

XX AEA81248;

DT 25-AUG-2005 (first entry)

XX Human angiotensin 1 (ANGPT1), transcript variant 2 protein.

XX screening; obesity; nutritional disorder; anorectic; angiotensin 1;
 XX ANGPT1; transcript variant.

XX Homo sapiens.

XX US2005136465-A1.

XX 23-JUN-2005.

XX 22-DEC-2004; 2004US-00019829.

XX 22-DEC-2003; 2003EP-00104902.

XX (CLER/) CLER R G.

XX (DUCH/) DUCHATEAU-NGUYEN G.

XX (GARD/) GARDEN C.

XX (MIZR/) MIZRAHI J.

XX (OSTE/) OSTENSON C.

XX Clerc RG, Duchateau-Nguyen G, Gardes C, Mizrahi J, Ostenson C;

XX WPI; 2005-457507/46.

XX N-PSDB; AEA81187.

XX Screening test compounds that reduce and/or prevent obesity involves
 XX contacting cell expressing gene from alpha-two-glycoprotein.

XX Claim 20; SEQ ID NO 115; 21pp; English.

XX The invention relates to a novel method for screening for test compounds
 XX that reduce and/or prevent obesity. The method comprises contacting a
 XX cell expressing a gene selected from SEQ ID NO. 1-12 or 25-85, with a
 XX compound. The method of the invention demonstrates anorectic applications
 XX and may be useful for screening for compounds that reduce and/or prevent
 XX obesity. The current sequence is that of the human angiotensin 1
 XX (ANGPT1), transcript variant 2 protein of the invention. The sequence
 XX listing for the specification can be located via the USPTO web-site.

XX Sequence 402 AA;

Query Match 100.0%; Score 106; DB 9; Length 402;
 Best Local Similarity 100.0%; Pred. No. 2.2e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLKGGKREBEKPF 20
 Db 264 LCTKEGVLKGGKREBEKPF 283

RESULT 11

ADSI3776

ID ADSI3776 standard; protein; 456 AA.

XX ADSI3776;

XX 02-DEC-2004 (first entry)

DE Mouse Ang-1 protein non-ECM-binding fragment.

XX Ang-1; extracellular matrix; ECM; angiotensin; cytostatic; vasotropic;
 XX antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;
 XX gene therapy; mouse.

XX Mus sp.

XX WO2004076650-A2.

XX 10-SEP-2004.

XX 27-FEB-2004; 2004WO-US006101.

XX 27-FEB-2003; 2003US-0450582P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Yu Q;

XX WPI; 2004-653413/63.

XX N-PSDB; ADSI3794.

XX New pharmaceutical composition comprises a pharmaceutical carrier and an
 XX amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein
 XX or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
 XX ischemia.

XX Claim 5; SEQ ID NO 8; 114pp; English.

XX The invention relates to a pharmaceutical composition comprising a
 XX pharmaceutical carrier and an amount of an extracellular matrix (ECM)-
 XX binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also
 XX provided are methods of treating an individual suspected of having
 XX coronary artery disease, vascular disease or a condition involving
 XX ischemia; of promoting angiogenesis, endothelial survival and
 XX maintaining vascular integrity in an individual; of treating an
 XX individual suspected of having a disease related to lack of blood vessels
 XX to effectively promote angiogenesis in the patients with the diseases
 XX related to lack of blood vessels such as ischemia in hearts and limbs;
 XX to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
 XX atherosclerosis risk by maintaining the health and integrity of blood
 XX vessels; to assist the recovery of the patients who had stroke and the
 XX angioplasty procedure by promoting the growth/survival of endothelial
 XX cells and establish endothelial monolayer and inhibit excessive
 XX inflammation, haemorrhage, and proliferation of vascular smooth muscle;
 XX to treat patients with restenosis by inhibiting re-closure of blood
 XX vessel after inserting stents into blood vessels; to make stable and
 XX functional artificial blood vessels comprising using the composition
 XX above; of identifying compounds that modulates binding of Ang-1 to ECM;
 XX of treating an individual suspected of having cancer; of preventing
 XX diabetes and/or arthritis in an individual suspected of being at risk of
 XX developing diabetes or arthritis. The pharmaceutical composition is
 XX useful for treating diseases and disorders, e.g. cancer, coronary artery
 XX disease, vascular disease, ischemia, restenosis, diabetes, stroke,
 XX angiogenesis, or arthritis. The present sequence represents a non-ECM-
 XX binding fragment of Ang-1 protein.

XX Sequence 456 AA;

```
Query Match      100.0%; Score 106; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20
    |||||
DB 222 LCTKEGVLLKGGKREBEKPF 241

RESULT 12
ID ADS13775
XX ADS13775 standard; protein; 456 AA.
AC ADS13775;
XX
XX
XX 02-DEC-2004 (first entry)
XX Human Ang-1 protein non-ECM-binding fragment.
DE
DE
XX Ang-1; extracellular matrix; ECM; angiotensin; cytotatic; vasotropic;
KW antidiabetic; antiarthritic; cerebroprotective; angiogenic;
KW gene therapy; human.
XX
XX Homo sapiens.
XX WO2004076650-A2.
XX
XX 10-SEP-2004.
XX
XX 27-FEB-2004; 2004WO-US006101.
XX
XX 27-FEB-2003; 2003US-0450582P.
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Yu Q;
XX WPI; 2004-653413/63.
DR N-PSDB; ADS13793.
XX
XX New pharmaceutical composition comprises a pharmaceutical carrier and an
PT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein
PT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
PT ischemia.
XX
XX Claim 5; SEQ ID NO 7; 114pp; English.
XX
XX The invention relates to a pharmaceutical composition comprising a
CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-
CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also
CC provided are methods of treating an individual suspected of having
CC coronary artery disease, vascular disease or a condition involving
CC ischaemia; of promoting angiogenesis, endothelial survival and
CC maintaining vascular integrity in an individual; of treating an
CC individual suspected of having a disease related to lack of blood vessels
CC to effectively promote angiogenesis in the patients with the diseases
CC related to lack of blood vessels such as ischaemia in hearts and limbs;
CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
CC atherosclerosis risk by maintaining the health and integrity of blood
CC vessels; to assist the recovery of the patients who had stroke and the
CC angioplasty procedure by promoting the growth/survival of endothelial
CC cells and establish endothelial monolayer and inhibit excessive
CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;
CC to treat patients with restenosis by inhibiting re-closure of blood
CC vessel after inserting stents into blood vessels; to make stable and
CC functional artificial blood vessels comprising using the composition
CC above; of identifying compounds that modulates binding of Ang-1 to ECM;
CC of treating an individual suspected of having cancer; of preventing
CC diabetes and/or arthritis in an individual suspected of being at risk of
CC developing diabetes or arthritis. The pharmaceutical composition is
CC useful for treating diseases and disorders, e.g. cancer, coronary artery
CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
CC angiogenesis, or arthritis. The present sequence represents a non-ECM-
CC
```

```
CC binding fragment of Ang-1 protein.
XX
SQ Sequence 456 AA;

Query Match      100.0%; Score 106; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20
    |||||
DB 222 LCTKEGVLLKGGKREBEKPF 241

RESULT 13
AAW47526
ID AAW47526 standard; protein; 494 AA.
XX
XX AAW47526;
AC AAW47526;
XX
XX 09-SEP-1998 (first entry)
DT
XX Amino acid sequence of chimeric TIE ligand 2N1C1F (chimera 4).
DE
XX Chimeric TIE ligand 2N1C1F; TIE-2 ligand; neovascularisation; tumour;
KW human.
XX
XX Homo sapiens.
OS
XX WO9805779-A1.
PN
XX 12-FEB-1998.
PD
XX 01-AUG-1997; 97WO-US013557.
XX
XX 02-AUG-1996; 96US-0022999P.
PR
XX 25-OCT-1996; 96US-00740223.
PR
XX (REGE-) REGENERON PHARM INC.
PA
XX Davis S, Yancopoulos GD;
PI WPI; 1998-145615/13.
XX N-PSDB; AAV18613.
XX
XX Modified human TIE-2 receptor ligand(s) - useful for promoting wound
PT healing.
PT
XX Claim 20; Fig 27; 202pp; English.
XX
XX This is the amino acid sequence of the chimeric TIE ligand 2N1C1F, used
CC in the method of the invention, involving the production of TIE-2 ligands
CC which promote healing. The nucleic acids, vectors and host cells used in
CC the method of the invention are useful for the recombinant production of
CC the ligands. The ligands, etc. are useful for blocking blood vessel
CC growth, promoting neovascularisation, promoting the growth or
CC differentiation of a cell expressing the TIE receptor, blocking the
CC growth or differentiation of a cell expressing the TIE receptor and for
CC attenuating or preventing tumour growth in a human
XX
XX Sequence 494 AA;
SQ

Query Match      100.0%; Score 106; DB 2; Length 494;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20
    |||||
DB 260 LCTKEGVLLKGGKREBEKPF 279

RESULT 14
AAR94603
ID AAR94603 standard; protein; 498 AA.
```



```

XX AAR94603;
XX AC
XX 28-OCT-1996 (first entry)
XX DT
XX DE Human TIE-2 ligand 1 derived from lambda-gt10 clone.
XX DX
XX KW Angiogenesis; neovascularisation; tumour development; wound healing; TIE;
XX KW tyrosine kinase with Ig and EGF homology domains; vector; recombinant;
XX KW clone; diagnosis; ischaemia; thromboembolytic disease; atherosclerosis;
XX KW inflammation; diabetes; ligand bodies; delivery; targeting.
XX OS
XX XX Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX XX Modified-site 269
XX FT /note= "extra Gly residue not present in TIE-2 ligand 1
XX FT derived from T98G clone (see AAT14649 and AAR94604)"
XX PN
XX XX WO9611269-A2.
XX XX
XX PD 18-APR-1996.
XX XX
XX XX 06-OCT-1995; 95WO-US012935.
XX XX
XX XX 07-OCT-1994; 94US-00319932.
XX XX 27-OCT-1994; 94US-00330261.
XX XX 08-DEC-1994; 94US-00348492.
XX XX 09-DEC-1994; 94US-00353503.
XX XX 17-JAN-1995; 95US-00373579.
XX XX 06-APR-1995; 95US-00418595.
XX XX
XX XX (REG-) REGENERON PHARM INC.
XX XX
XX PI Davis S, Bruno J, Goldfarb M, Aldrich TH, Maisompierre PC;
XX PI Radziejewski C, Jones PF, Yancopoulos GD;
XX XX
XX DR WPI; 1996-209850/21.
XX DR N-PSDB; AAT14648.
XX XX
XX XX Nucleic acid encoding TIE-2 ligand and related vectors - useful in
XX PT diagnosis and treatment of neovascularisation, tumours, etc., or to
XX PT promote wound healing, etc.
XX XX
XX PS Claim 2; Fig 4; 84pp; English.
XX XX
XX XX AAR94603 is a recombinant human TIE-2 (hTIE-2) ligand 1 derived from a
XX CC lambda-gt10 clone. The ligand has an extra Gly residue (aa 269) as
XX CC compared to the hTIE-2 ligand from a T98G clone (see AAT14649 and
XX CC AAR94604). hTIE-2 ligand DNAs of the invention are recombinant versions
XX CC of the native ligand coding sequences and may be used to produce the
XX CC ligands at a high yield. Antibodies and receptor bodies that bind to TIE-
XX CC 2 ligands may be used to inhibit angiogenesis and neovascularisation
XX CC (e.g. associated with tumour development) and the TIE-2 ligands
XX CC themselves are useful to promote neovascularisation and wound healing
XX CC e.g. for treatment of ischaemia. TIE-2 ligands are also useful to treat
XX CC thromboembolytic disease, atherosclerosis, inflammation and diabetes.
XX CC Ligand bodies contg. TIE-2 ligands may also be useful for the delivery
XX CC and targeting of growth factors, toxins etc. to sites where their
XX CC presence is advantageous
XX XX
XX SQ Sequence 498 AA;
XX
XX Query Match 100.0%; Score 106; DB 2; Length 498;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-08;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LCTKEGVLKGGKREKPF 20
XX |
XX Db 264 LCTKEGVLKGGKREKPF 283
XX |

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AAW01409
ID AAW01409 standard; protein; 498 AA.
XX AC
XX AAW01409;
XX DT
XX 11-FEB-1997 (first entry)
XX DE
XX Human TIE-2 ligand 1 (lambda-gt10 clone product).
XX KW TIE-2 ligand 1; tyrosine kinase with Ig and EGF homology domain;
XX KW receptor; agonist; neovascularisation; wound healing; ischaemia;
XX KW leukopaenia; thrombocytopaenia; anaemia; angiogenesis; tumour;
XX KW atherosclerosis; inflammation; diagnosis; therapy.
XX OS
XX XX Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX XX Misc-difference 269
XX FT /note= "Gly-269 is absent in TIE-2 ligand 1 from
XX FT glioblastoma T98G"
XX XX
XX PN WO9631598-A1.
XX XX
XX PD 10-OCT-1996.
XX XX
XX XX 05-APR-1996; 96WO-US004806.
XX XX
XX XX 06-APR-1995; 95US-00418595.
XX PR 06-OCT-1995; 95WO-US012935.
XX XX
XX XX (REG-) REGENERON PHARM INC.
XX XX
XX PI Davis S, Bruno J, Goldfarb M, Aldrich TH, Maisompierre PC;
XX PI Radziejewski C, Jones PF, Yancopoulos GD;
XX XX
XX DR WPI; 1996-465021/46.
XX DR N-PSDB; AAT44319.
XX XX
XX XX TIE-2 agonists and antagonists and related DNA - useful for promoting or
XX PT blocking neovascularisation, etc.
XX XX
XX PS Claim 14; Fig 4; 113pp; English.
XX XX
XX CC Human TIE-2 (tyrosine kinase with Ig and EGF homology domains) ligand 1
XX CC (AAW01409) is a ligand that binds the TIE-2 receptor. Its amino acid
XX CC sequence was deduced from a cDNA clone (AAT44319) derived from foetal
XX CC lung cells. A variant form of the ligand (AAW01410), lacking Gly-269, is
XX CC produced by a cDNA clone (AAT44320) from glioblastoma T98G cells. Both
XX CC ligands are TIE-2 agonists useful in promoting the growth, survival,
XX CC migration and/or differentiation and/or stabilisation or destabilisation
XX CC of cells expressing the TIE-2 receptor. They can be isolated from natural
XX CC sources or produced in transformed host cells
XX XX
XX SQ Sequence 498 AA;
XX
XX Query Match 100.0%; Score 106; DB 2; Length 498;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-08;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LCTKEGVLKGGKREKPF 20
XX |
XX Db 264 LCTKEGVLKGGKREKPF 283
XX |

```

Search completed: May 11, 2006, 11:33:14
Job time : 185 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 11:33:31 ; Search time 38 Seconds
(without alignments)
50.640 Million cell updates/sec

Title: US-10-789-222-1
Perfect score: 106
Sequence: 1 LCTKEGVLLKGGKREBEKPF 20
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	49	46.2	658	2 B86599	metal transport p-
2	49	46.2	658	2 D72026	metal transport p-
3	49	46.2	659	2 A81742	cation-transportin
4	49	46.2	659	2 B71479	probable metal tra
5	49	46.2	683	2 C81515	cation-transportin
6	47	44.3	673	2 AG3521	cation-transportin
7	47	44.3	927	1 JQ0948	A5 antigen precurs
8	46.5	43.9	591	1 SVHUTP	CTP synthase (SC 6
9	45	43.4	389	2 S01371	myosin heavy chain
10	45	42.5	168	2 JG0184	fibroblast growth
11	45	42.5	257	2 E71601	probable integral
12	45	42.5	450	2 S15675	globulin-2 precurs
13	44	41.5	97	2 T29766	hypothetical prote
14	44	41.5	141	2 T48751	hypothetical prote
15	44	41.5	154	2 T20508	hypothetical prote
16	44	41.5	228	2 C87184	conserved hypothet
17	44	41.5	281	2 B81440	acetylglutamate ki
18	44	41.5	396	2 A48336	coat protein - Sou
19	44	41.5	406	1 A70015	probable NADH2 deh
20	44	41.5	486	2 S63384	hypothetical prote
21	43	40.6	216	2 A56861	peptidylprolyl iso
22	43	40.6	227	2 F90249	ribose 5-phosphate
23	43	40.6	394	2 H97825	elongation factor
24	43	40.6	394	2 C71672	translation elonga
25	43	40.6	416	2 H69436	5-enolpyruvylshiki
26	43	40.6	477	2 T52382	zinc finger protei
27	43	40.6	504	2 T10898	legumin-like prote
28	43	40.6	590	2 C81911	nitrate/nitrite se
29	43	40.6	590	2 B81104	nitrate/nitrite se

30	43	40.6	1792	2 T08878	supervillin P205 -
31	42.5	40.1	71	2 C82807	30S ribosomal prot
32	42.5	40.1	204	2 E64507	molybdopterin-guan
33	42.5	40.1	284	2 F71091	hypothetical prote
34	42	39.6	134	2 S39046	phosphoneuroprotei
35	42	39.6	137	2 I56498	phosphoneuroprotei
36	42	39.6	140	2 A49669	synuclein alpha -
37	42	39.6	149	2 B43959	synuclein, form 2
38	42	39.6	187	2 S10721	cathepsin D inhibi
39	42	39.6	188	1 XKPODC	cathepsin D inhibi
40	42	39.6	220	1 XKPOD	aspartic proteinas
41	42	39.6	220	2 S52656	cathepsin D inhibi
42	42	39.6	220	2 S24186	aspartic proteinas
43	42	39.6	221	2 T07411	proteinase inhibit
44	42	39.6	221	2 T07413	proteinase inhibit
45	42	39.6	221	2 JQ2246	22.5K cathepsin D

ALIGNMENTS

RESULT 1

B86599
metal transport P-type ATPase [imported] - Chlamydomophila pneumoniae (strain J138)
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86599
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: B86599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-658 <STO>
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:BA000008; NID:G8979242; PFI
A;Experimental source: strain J138
C;Genetics:
A;Gene: zntA
C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d

Query Match 46.2%; Score 49; DB 2; Length 658;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CTKEGVLLKGG 12
| | | | | | | | | |
Db 331 CAKHGVLLKGG 341

RESULT 2

D72026
metal transport P-type ATPase - Chlamydomophila pneumoniae (strain CWL029)
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: D72026
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: D72026
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-658 <ARN>
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001667; GB:AE001363; NID:
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: zntA
C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d

Query Match 46.2%; Score 49; DB 2; Length 658;
Best Local Similarity 81.8%; Pred. No. 16;

```

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTKEGVLLKGG 12
| . . . . .
Db 331 CAXHGVLLKGG 341

RESULT 3
A81742
cation-transporting ATPase, E1-E2 family TC0100 [imported] - Chlamydia muridarum (strain
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: A81742
R;Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: A81742
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-659 <TET>
A;Cross-references: UNIPROT:Q9PLJ9; UNIPARC:UPI00000577C9; GB:AE002277; GB:AE002160; NID
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0100
C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
F;478-620/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 46.2%; Score 49; DB 2; Length 659;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTKEGVLLKGG 12
| . . . . .
Db 331 CAXHGVLLKGG 341

RESULT 4
B71479
probable metal transport p-type ATPase - Chlamydia trachomatis (serotype D, strain UW3/C
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: B71479
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: B71479
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-659 <ARN>
A;Cross-references: UNIPROT:O84732; UNIPARC:UPI00000D3395; GB:AE001343; GB:AE001273; NID
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: zntA
C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
F;64-400/Domain: ATPase transduction domain homology <ATN>
F;478-620/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 46.2%; Score 49; DB 2; Length 659;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTKEGVLLKGG 12
| . . . . .
Db 331 CAXHGVLLKGG 341

RESULT 5
C81515
cation-transporting ATPase, E1-E2 family CP1001 [imported] - Chlamydophila pneumoniae (s
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

```

```

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81515
R;Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: C81515
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-683 <REA>
A;Cross-references: UNIPROT:Q9K1U0; UNIPARC:UPI00000CCCD4; GB:AE002257; GB:AE002161; NID
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP1001
C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
F;503-645/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 46.2%; Score 49; DB 2; Length 683;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTKEGVLLKGG 12
| . . . . .
Db 356 CAXHGVLLKGG 366

RESULT 6
AG3521
cation-transporting p-type ATPase b (EC 3.6.1.-) [imported] - Brucella melitensis (strain
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AG3521
R;DelVecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.;
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesee
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis;
A;Reference number: AD3252; PMID:11756688
A;Accession: AG3521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-673 <KUR>
A;Cross-references: UNIPROT:Q8YDS8; UNIPARC:UPI0000058350; GB:AE008918; PIDN:AAL53338.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI0097
A;Map position: 11
C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
C;Keywords: hydrolase

Query Match 44.3%; Score 47; DB 2; Length 673;
Best Local Similarity 56.2%; Pred. No. 33;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREE 16
| . . . . .
Db 337 VCARGVLLKGGKALE 352

RESULT 7
JQ0948
A5 antigen precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JH0466; JQ0948
R;Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
A;Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology
A;Reference number: JH0466; MUID:91337458; PMID:1908252
A;Accession: JH0466
A;Molecule type: mRNA
A;Residues: 1-927 <TAK>
A;Cross-references: UNIPARC:UPI0000171502; GB:D10467; GB:D01077; NID:g222962; PIDN:BAA011

```

A;Status: not compared with conceptual translation

A:Molecule type: mRNA
A;Residues: 36-389 <CAS2>
A;Cross-references: UNIPARC:UPI0000177609
A;Note: the sequence from fig. 7 is inconsistent with that from fig. 5 in having 64-Ile,
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP; cardiac muscle; coiled coil; heart; muscle contraction; skeletal muscle

Query Match 43.4%; Score 46; DB 2; Length 389;
Best Local Similarity 44.4%; Pred. No. 28;
Matches 8; Conservative 5; Mismatches 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREEEK 18
| : : : : :
Db 249 LMEAEQIAMRGKKQEOK 266

RESULT 10

JG0184
fibroblast growth factor - human
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: JG0184
R;Xok, L.D.S.; Teui, S.K.W.; Waye, M.; Liew, C.C.; Lee, C.Y.; Fung, K.P.
Biochem. Biophys. Res. Commun. 255 717-721, 1999
A;Title: Cloning and characterization of a cDNA encoding a novel fibroblast growth factor
A;Reference number: JG0184; MUID:99160419; PMID:10049777
A;Accession: JG0184
A;Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-168 <KOK>
A;Cross-references: UNIPROT:P61328; UNIPARC:UPI0000040663; GB:U76381
C;Superfamily: fibroblast growth factor

Query Match 42.5%; Score 45; DB 2; Length 168;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 4; Mismatches 0; Gaps 0;

QY 4 KEGVLLKGGKREEEKP 19
||| : || : ||
Db 117 KEGQIMKGNRVETKP 132

RESULT 11

E71601
probable integral membrane protein PFB0995W - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Accession: E71601
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Pertera, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: E71601
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A;Residues: 1-257 <GAR>
A;Cross-references: UNIPROT:Q9TY93; UNIPARC:UPI00000814CB; GB:AE001431; GB:AE001362; NID
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0995W

Query Match 42.5%; Score 45; DB 2; Length 257;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 11; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 4 KEGVLLK-----GGKREEEKP 19
| | | | | | : : : : :
Db 11 KSGVLLKDKNTEGRKKERQKP 32

RESULT 12

S15675
Globulin-2 precursor - maize
C/Species: Zea mays (maize)
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S15675
R/Wallace, N.H.; Kriz, A.L.
Plant Physiol. 95, 973-975, 1991
A/Title: Nucleotide sequence of a cDNA clone corresponding to the maize globulin-2 gene.
A/Reference number: S15675
A/Accession: S15675
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-450 <WAL>
A/Cross-references: UNIPROT:Q7M1Z8; UNIPARC:UPI0000177E41
C/Superfamily: vicilin

Query Match 42.5%; Score 45; DB 2; Length 450;
Best Local Similarity 68.8%; Pred. No. 45;
Matches 11; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

QY 4 KEG----VLLKGGKRE 15
||| |||:|||||
Db 95 KEGGVIVLLGGKRE 110

RESULT 13
T29766
hypothetical protein ZC581.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T29766
R/Waterston, B.; Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, May 1997
A/Description: The sequence of C. elegans cosmid ZC581.
A/Reference number: Z20682
A/Accession: T29766
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-97 <WAT>
A/Cross-references: UNIPARC:UPI000017BCE4; EMBL:AF003134; PIDN:AAB54143.1; GSPDB:GN00019
A/Experimental source: strain Bristol N2; clone ZC581
C/Genetics:
A/Gene: ZC581.5
A/Map position: 1
A/Introns: 74/1

Query Match 41.5%; Score 44; DB 2; Length 97;
Best Local Similarity 53.8%; Pred. No. 15;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 EGVLKGGKRE 17
|:|||||:
Db 31 ERIMKGGKNEED 43

RESULT 14
T48751
hypothetical protein 8D4.250 [imported] - Neurospora crassa
C/Species: Neurospora crassa
C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
C/Accession: T48751
R/Schulte U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, April 2000
A/Reference number: Z24541
A/Accession: T48751
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-141 <SCH>
A/Cross-references: UNIPARC:UPI0000179478; EMBL:AL353819; GSPDB:GN00112; NCSP:8D4.250
A/Experimental source: cosmid contig 8D4; strain 74
C/Genetics:
A/Gene: NCSP:8D4.250
A/Map position: 2

C/Superfamily: Neurospora crassa hypothetical protein 8D4.250

Query Match 41.5%; Score 44; DB 2; Length 141;
Best Local Similarity 64.3%; Pred. No. 21;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 TKEGVLLKGGKRE 16
||| |||:|||||
Db 74 TRNGKLLSGKDED 87

RESULT 15
T20508
hypothetical protein F02E9.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T20508
R/Gray, I.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19285
A/Accession: T20508
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-154 <WIL>
A/Cross-references: UNIPROT:O01314; UNIPARC:UPI0000074F98; EMBL:Z81494; PIDN:CAB04047.1;
A/Experimental source: clone F02E9
C/Genetics:
A/Gene: CESP:F02E9.1
A/Map position: 1
A/Introns: 29/2; 52/2; 80/3; 131/3

Query Match 41.5%; Score 44; DB 2; Length 154;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 12; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 LCTKEG--VLLKGGKRE 18
||| |||:|||||
Db 53 LDTKNGKGVLLKKNSENEEK 72

Search completed: May 11, 2006, 11:37:58
Job time : 39 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 11:30:26 ; Search time 234 Seconds
(without alignments)
60.302 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLKGGKREBEKPF 20

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	106	100.0	159	2	Q5YLW1_HUMAN	Q5YLW1 homo sapien
2	106	100.0	498	1	ANGPI_HUMAN	Q15389 homo sapien
3	106	100.0	498	1	ANGPI_MOUSE	Q08538 mus musculus
4	106	100.0	498	2	Q5HYA0_HUMAN	Q5HYA0 homo sapien
5	106	100.0	498	2	Q6NWV7_MOUSE	Q6NWV7 mus musculus
6	106	100.0	498	2	Q8C2K6_MOUSE	Q8C2K6 mus musculus
7	96	90.6	498	2	Q9BDY8_FIG	Q9BDY8 sus scrofa
8	89.5	84.4	147	2	Q8N6P3_HUMAN	Q8N6P3 homo sapien
9	89.5	84.4	497	1	ANGPI_RAT	Q35460 rattus norv
10	89.5	84.4	521	2	Q6A0F0_MOUSE	Q6A0F0 mus musculus
11	86.5	81.6	497	2	Q60FC1_CANFA	Q60FC1 canis famil
12	85.5	80.7	481	1	ANGPI_BOVIN	Q18920 bos taurus
13	76	71.7	504	2	Q6GNY4_XENLA	Q6GNY4 xenopus lae
14	59	55.7	383	2	Q9CUL6_MOUSE	Q9CUL6 mus musculus
15	55	51.9	178	2	Q4RNQ8_TETNG	Q4RNQ8 tetraodon n
16	54	50.9	1040	2	Q8H7M2_ORYSA	Q8H7M2 oryza sativ
17	53	50.0	890	2	Q8B488_9FLAV	Q8B488 ignape viru
18	52.5	49.5	591	2	Q5XHA8_XENLA	Q5XHA8 xenopus lae
19	51	48.1	181	2	Q816J1_CIOSA	Q816J1 clona savig
20	51	48.1	273	2	Q9CST2_MOUSE	Q9CST2 mus musculus
21	51	48.1	566	2	Q7Y188_ORYSA	Q7Y188 oryza sativ
22	51	48.1	691	2	Q7Y017_ORYSA	Q7Y017 oryza sativ
23	51	48.1	940	2	Q7XDX7_ORYSA	Q7XDX7 oryza sativ
24	51	48.1	974	2	Q6L4Z3_ORYSA	Q6L4Z3 oryza sativ
25	51	48.1	982	2	Q7XWN4_ORYSA	Q7XWN4 oryza sativ
26	51	48.1	1059	2	Q60E55_ORYSA	Q60E55 oryza sativ
27	51	48.1	1109	2	Q5KQJ6_ORYSA	Q5KQJ6 oryza sativ
28	51	48.1	1177	2	Q75J33_ORYSA	Q75J33 oryza sativ
29	51	48.1	1180	2	Q75HC1_ORYSA	Q75HC1 oryza sativ
30	51	48.1	1198	2	Q6L5S9_ORYSA	Q6L5S9 oryza sativ
31	51	48.1	1198	2	Q94GS7_ORYSA	Q94GS7 oryza sativ

ALIGNMENTS

RESULT 1

Q5YLW1_HUMAN PRELIMINARY; PRT; 159 AA.
AC Q5YLW1;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Angiopoietin-A.
GN Name=AngA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang H., Zhang Y., Liang H.C., Zhang M., Sun D.H., Wang B.,
RA Zhang G.Z.;
RT "The Expression of Angiopoietin-A During Vascular Development.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055342; AAL59669.1; -; mRNA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C.1;
SQ SEQUENCE 159 AA; 18221 MW; F129DA56FB6AFCC6 CRC64;

Query Match 100.0%; Score 106; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLKGGKREBEKPF 20
|||
Db 77 LCTKEGVLKGGKREBEKPF 96

RESULT 2

ANGPI_HUMAN STANDARD; PRT; 498 AA.
AC Q15389;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1).
GN Name=ANGPT1; Synonyms=KIAA00003;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.
RC TISSUE=Fetal lung;
RX MEDLINE=97134663; PubMed=8980223; DOI=10.1016/S0092-8674(00)81812-7;
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maissonpierre P.C.,

32 51 48.1 1224 2 Q84TW9_ORYSA Q84TW9 oryza sativ
33 51 48.1 1225 2 Q5TKC1_ORYSA Q5TKC1 oryza sativ
34 51 48.1 1229 2 Q6I578_ORYSA Q6I578 oryza sativ
35 51 48.1 1264 2 Q7XP54_ORYSA Q7XP54 oryza sativ
36 51 48.1 1264 2 Q8LSK0_MAIZE Q8LSK0 zea mays (m
37 51 48.1 1274 2 Q9FW32_ORYSA Q9FW32 oryza sativ
38 51 48.1 1277 2 Q53KA0_ORYSA Q53KA0 oryza sativ
39 51 48.1 1282 2 Q7XRW0_ORYSA Q7XRW0 oryza sativ
40 51 48.1 1289 2 Q60E18_ORYSA Q60E18 oryza sativ
41 51 48.1 1297 2 Q6L563_ORYSA Q6L563 oryza sativ
42 51 48.1 1297 2 Q7X563_ORYSA Q7X563 oryza sativ
43 51 48.1 1297 2 Q6L4G8_ORYSA Q6L4G8 oryza sativ
44 51 48.1 1302 2 Q6L5B9_ORYSA Q6L5B9 oryza sativ
45 51 48.1 1302 2 Q75J10_ORYSA Q75J10 oryza sativ

RA Yancopoulos G.D.;
RT "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by
RL secretion-trap expression cloning."; Cell 87:1161-1169(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.
RA Nakatekasa M., Komai K., Shiozawa S.;
RT "Human angiopoietin-1 mRNA variant form.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.
RA Shan Z.X., Yu X.Y., Lin Q.Y., Fu Y.H., Tan H.H., Zheng M., Lin S.G.;
RT "Human angiopoietin-1 mRNA variant forms.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Bone marrow;
RX MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1."; DNA Res. 1:27-35(1994).
RN [5]
RP SEQUENCE REVISION.
RX MEDLINE=22158633; PubMed=12168954;
RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
RT "Construction of expression-ready cDNA clones for KIAA genes: manual
RT curation of 330 KIAA cDNA clones."; DNA Res. 9:99-106(2002).
RL CNA Res. 9:99-106(2002).
CC -1- FUNCTION: Binds and activates TIE2 receptor by inducing its
CC tyrosine phosphorylation. Implicated in endothelial developmental
CC processes later and distinct from that of VEGF. Appears to play a
CC crucial role in mediating reciprocal interactions between the
CC endothelium and surrounding matrix and mesenchyme. Mediates blood
CC vessel maturation/stability. It may play an important role in the
CC heart early development.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Glycosylated.
CC -1- MISCELLANEOUS: It may have a potential therapeutic utility since
CC it can be used for specifically targeting tumor vasculature or for
CC promoting angiogenic processes in certain organs such as an
CC ischemic heart.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC ENBL; U83508; AAB50557.1; -; mRNA.
DR ENBL; AB084454; BAB91325.1; -; mRNA.
DR ENBL; AV121504; AAM81745.1; -; mRNA.
DR ENBL; AV124380; AAM92271.1; -; mRNA.
DR ENBL; D13628; BAA02793.2; ALT_INIT; mRNA.
DR HSP; P02671; IPZD.
DR Ensembl; ENSG00000154188; Homo sapiens.
DR HGNC; HGNC:484; ANGPT1.
DR H-InvDB; HIX000720; -.
DR MIM; 601667; -.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FEG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;
KM Glycoprotein; Polymorphism; Signal.
FT SIGNAL 1 15 Potential.
FT CHAIN 16 498 Angiopoietin-1.

FT DOMAIN 284 498 Fibrinogen C-terminal.
FT COILED 81 119 Potential.
FT COILED 153 261 Potential.
FT CARBOHYD 92 92 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 154 154 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 243 243 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 295 295 N-linked (GlcNAc...) (Potential).
FT DISULFID 286 315 By similarity.
FT DISULFID 439 452 Missing (in cell line T98G; may be due to
FT VARIANT 269 exon slippage).
FT SQ SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;
/FTID=VAR_009940.
Query Match 100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LCTKGVLLKGGKREKDP 20
DB 264 LCTKGVLLKGGKREKDP 283
|||||
RESULT 3
ANGP1_MOUSE STANDARD; PRT; 498 AA.
AC O08538;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1).
GN Name-Angpt1; Synonyms-Agpt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97134663; PubMed=8980223; DOI=10.1016/S0092-8674(00)81812-7;
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maisonpierre P.C.,
RA Yancopoulos G.D.;
RT "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by
RT secretion-trap expression cloning."; Cell 87:1161-1169(1996).
RL [1]
CC -1- FUNCTION: Binds and activates TIE2 receptor by inducing its
CC tyrosine phosphorylation. Implicated in endothelial developmental
CC processes later and distinct from that of VEGF. Appears to play a
CC crucial role in mediating reciprocal interactions between the
CC endothelium and surrounding matrix and mesenchyme. Mediates blood
CC vessel maturation/stability. It may play an important role in the
CC heart early development.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: Early in development, at E9 to E11, it is
CC found most prominently in the heart myocardium surrounding the
CC endocardium. Later, it becomes more widely distributed, most often
CC in the mesenchyme surrounding developing vessels, in close
CC association with endothelial cells.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC ENBL; U83509; AAB50558.1; -; mRNA.
DR HSP; P02671; IPZD.
DR Ensembl; ENSMUSG0000022309; Mus musculus.
DR MGI; MGI:108448; Angpt1.
DR GO; GO:0005615; Extracellular space; TAS.

DR GO; GO:0005172; F:vascular endothelial growth factor receptor. . . ; TAS.
 DR GO; GO:0007492; P:endoderm development; TAS.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;
 KW Glycoprotein; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 498 Angiopoietin-1.
 FT DOMAIN 284 498 Fibrinogen C-terminal.
 FT COILED 81 119 Potential.
 FT COILED 153 261 Potential.
 FT CARBOHYD 92 92 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 122 122 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 154 154 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 243 243 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 295 295 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 286 315 By similarity.
 FT DISULFID 439 452 By similarity.
 SQ SEQUENCE 498 AA; 57505 MW; 285B4FDEC260D800 CRC64;
 Query Match 100.0%; Score 106; DB 1; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LCTKEGVLKGGKREKEKPF 20
 DB 264 LCTKEGVLKGGKREKEKPF 283
 RESULT 4
 QSHYAO HUMAN
 ID QSHYAO HUMAN PRELIMINARY; PRT; 498 AA.
 AC QSHYAO
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein DKFZp686L10222.
 GN Name=DKFZp686L10222;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Small intestine;
 RG The German cDNA Consortium;
 RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
 RA Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX648814; CAI45984.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;
 Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LCTKEGVLKGGKREKEKPF 20
 DB 264 LCTKEGVLKGGKREKEKPF 283
 RESULT 5
 Q6NNV7 MOUSE
 ID Q6NNV7 MOUSE PRELIMINARY; PRT; 498 AA.
 AC Q6NNV7
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 QY 1 LCTKEGVLKGGKREKEKPF 20
 DB 264 LCTKEGVLKGGKREKEKPF 283
 Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LCTKEGVLKGGKREKEKPF 20
 DB 264 LCTKEGVLKGGKREKEKPF 283
 Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LCTKEGVLKGGKREKEKPF 20
 DB 264 LCTKEGVLKGGKREKEKPF 283

DE Angiopoietin 1.
 GN Name=Angptl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wegner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Jordan H., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadin T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RA Director MGC Project;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC067410; AAH67410.1; -; mRNA.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005172; F:vascular endothelial growth factor receptor. . . ; TAS.
 DR GO; GO:0007492; P:endoderm development; TAS.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 498 AA; 57519 MW; FC36F905A9E79074 CRC64;
 Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LCTKEGVLKGGKREKEKPF 20
 DB 264 LCTKEGVLKGGKREKEKPF 283
 RESULT 6
 Q8C2K6 MOUSE
 ID Q8C2K6 MOUSE PRELIMINARY; PRT; 498 AA.
 AC Q8C2K6
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 2 days neonate thymic cells cDNA, RIKEN full-
 DE length enriched library, clone:E430016L03 product:angiopoietin, full
 DE insert sequence.
 GN Name=Angptl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=99279233; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Kasavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagata S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama N., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akamura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirokawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK088439; BAC40354.1; -; mRNA.
DR HSSP; P02671; 1PZD.
DR MGI; MGI:108448; Angpt1.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C.1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.
SQ SEQUENCE 498 AA; 57475 MW; 285D957468C5D800 CRC64;
Query Match 100.0%; Score 106; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.8e-07; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 1 LCTKEGVLLGKGRKEPKF 20
Db 264 LCTKEGVLLGKGRKEPKF 283
|||||
RESULT 7
Q9BDY8_PIG PRELIMINARY; PRT; 498 AA.
ID Q9BDY8_PIG PRELIMINARY; PRT; 498 AA.
AC Q9BDY8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Angiopoietin 1.
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21153163; PubMed=11230987; DOI=10.1016/S0008-6363(00)00295-9;
RA Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;
RT "The angiopoietin-tie2 system in coronary artery endothelium prevents
RT oxidized low-density lipoprotein-induced apoptosis.";
RL Cardiovasc. Res. 49:872-881(2001).
DR EMBL; AF23227; AAK14992.1; -; mRNA.
DR HSSP; P02671; 1PZD.
DR GO; GO:0001525; P.angiogenesis; IEA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C.1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.
SQ SEQUENCE 498 AA; 57413 MW; A8C1C8BF56061876 CRC64;
Query Match 90.6%; Score 96; DB 2; Length 498;
Best Local Similarity 90.0%; Pred. No. 6e-06; Indels 0; Gaps 0;
Matches 18; Conservative 1; Mismatches 1;
QY 1 LCTKEGVLLGKGRKEPKF 20
Db 264 LCTKEGVLLGKGRKEPKF 283
|||||
RESULT 8
Q9N6P3_HUMAN PRELIMINARY; PRT; 147 AA.
ID Q9N6P3_HUMAN PRELIMINARY; PRT; 147 AA.
AC Q9N6P3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ANGPT1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; Feingold E.A., Grouse L.H., Derge J.G.,
RA Strauberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haiech P.,
RA Hopkins R.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Datschenko L., Matuszewska K., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan J.A., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Strauberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029406; AAH29406.1; -; mRNA.
DR HSPSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR Prosite; PS00514; FIBRIN AG_C_DOMAIN; 1.
DR Angiogenesis; Coiled coil; Developmental protein; Differentiation;
DR Glycoprotein; Signal.
SQ SEQUENCE 147 AA; 17314 MW; 68DFD40DE06FA37E CRC64;

Query Match 84.4%; Score 89.5; DB 2; Length 147;
Best Local Similarity 95.0%; Pred. No. 1.8e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LCTKEGVLLKGGKREEEKPF 20
| | | | | | | | | | | | | | | | | | | | | |
Db 10 LCTKE-VLLKGGKREEEKPF 28

RESULT 9
ANGP1 RAT STANDARD; PRT; 497 AA.
AC Q35460; Q8K404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1).
GN Name=Angpt1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar; TISSUE=Placenta;
RX MEDLINE=22346496; PubMed=12458684; DOI=10.1023/A:1020921818105;
RA Iizasa H., Bae S.H., Asashima T., Kitano T., Matsunaga N.,
RA Teraaki T., Kang Y.S., Nakaehima E.;
RT Augmented expression of the tight junction protein occludin in brain
RT endothelial cell line FR-BBB by rat angiotensin-1 expressed in
RT baculovirus-infected sf plus insect cells."
RL Pharm. Res. 19:1757-1760(2002).
[2]
RP NUCLEOTIDE SEQUENCE OF 91-200.
RC STRAIN=Sprague-Dawley; TISSUE=Placenta;
RX MEDLINE=98451564; PubMed=9776732;
RA Mandriota S.J., Pepper M.S.;

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RT "Regulation of angiotensin-2 mRNA levels in bovine microvascular
RT endothelial cells by cytokines and hypoxia.";
RL Circ. Res. 83:852-859(1998).
CC -1- FUNCTION: Binds and activates TIE2 receptor by inducing its
CC tyrosine phosphorylation. Implicated in endothelial developmental
CC processes later and distinct from that of VEGF. Appears to play a
CC crucial role in mediating reciprocal interactions between the
CC endothelium and surrounding matrix and mesenchyme. Mediates blood
CC vessel maturation/stability. It may play an important role in the
CC heart early development.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AB080023; BAC10290.1; -; mRNA.
CC EMBL; AF030376; AAC78246.1; -; mRNA.
CC HSPSP; P02671; 1FZD.
CC Ensembl; ENSRNOG0000005854; Rattus norvegicus.
CC RCD; 628896; Angpt1.
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0001525; P:angiogenesis; IEP.
CC GO; GO:0048014; P:Tie receptor signaling pathway; IDA.
CC InterPro; IPR002181; Fibrinogen_C.
CC Pfam; PF00147; Fibrinogen_C; 1.
CC SMART; SM00186; FBG; 1.
CC PROSITE; PS00514; FIBRIN AG_C_DOMAIN; 1.
CC Angiogenesis; Coiled coil; Developmental protein; Differentiation;
CC Glycoprotein; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 497 Angiopoietin-1.
FT DOMAIN 283 497 Fibrinogen C-terminal.
FT COILED 81 119 Potential.
FT COILED 153 261 Potential.
FT CARBOHYD 92 92 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 122 122 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 154 154 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 243 243 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 294 294 N-linked (GLCNAC. .) (Potential).
FT DISULFID 285 314 By similarity.
FT DISULFID 438 451 By similarity.
FT CONFLICT 98 98 Q -> E (in Ref. 2).
FT CONFLICT 172 172 E -> K (in Ref. 2).
FT CONFLICT 189 189 E -> K (in Ref. 2).
SQ SEQUENCE 497 AA; 57461 MW; 08E6A8B8F868AE CRC64;

Query Match 84.4%; Score 89.5; DB 1; Length 497;
Best Local Similarity 95.0%; Pred. No. 6e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LCTKEGVLLKGGKREEEKPF 20
| | | | | | | | | | | | | | | | | | | | | |
Db 264 LCTKE-VLLKGGKREEEKPF 282

RESULT 10
Q6A0F0 MOUSE
ID Q6A0F0 MOUSE PRELIMINARY; PRT; 521 AA.
AC Q6A0F0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MKIAA0003 protein (Fragment).
GN Name=Angpt1; Synonyms=mkIAA0003;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Adult spleen;
RX PubMed=15368895;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Saito S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT IV. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 11:205-218(2004).
DR EMBL; AK172868; BAD32146.1; -; mRNA.
DR MGI; MGI:108448; Angptl.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005172; F:vascular endothelial growth factor receptor. .; TAS.
DR GO; GO:0007492; P:endothelium development; TAS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
FT NON TER
SQ SEQUENCE 521 AA; 60103 MW; 8E7061F2A570EDFA CRC64;

Query Match 84.4%; Score 89.5; DB 2; Length 521;
Best Local Similarity 95.0%; Pred. No. 6.2e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 LCTKEGVLKGGKREBEKPF 20
DQ 288 LCTKE-VLLKGGKREBEKPF 306
||||| ||||||| |||||||

RESULT 11
Q60FC1 CANFA
ID Q60FC1 CANFA PRELIMINARY; PRT; 497 AA.
AC Q60FC1
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE Angiopoietin-1.
GN NamesAng-1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN NUCLEOTIDE SEQUENCE.
RA Kato Y., Asano K.;
RT "Canis familiaris Angiopoietin-1 mRNA, complete cds.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB192412; BAD54826.1; -; mRNA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 497 AA; 57415 MW; 061AFC2B03B8F081 CRC64;

Query Match 81.6%; Score 86.5; DB 2; Length 497;
Best Local Similarity 90.0%; Pred. No. 0.00017;
Matches 18; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 LCTKEGVLKGGKREBEKPF 20
DQ 264 LCTKE-VLLKGGKREBEKPF 282
||||| ||||||| |||||||

RESULT 12
ANGP1_BOVIN
ID ANGP1_BOVIN STANDARD; PRT; 481 AA.

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AC Q18920;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1) (Fragment).
GN Name=ANGPT1; Synonyms=ANG1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Ovary;
RX MEDLINE=99054348; PubMed=9840613;
RA Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
RT "Analysis of blood vessel maturation processes during cyclic ovarian
RT angiogenesis.";
RL Lab. Invest. 78:1385-1394(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 91-200.
RC TISSUE=Liver;
RX MEDLINE=98451564; PubMed=9776732;
RA Mandriota S.J., Pepper M.S.;
RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
RT endothelial cells by cytokines and hypoxia.";
RL Circ. Res. 83:852-859(1998).
CC -1- FUNCTION: Binds and activates TIE2 receptor by inducing its
CC tyrosine phosphorylation. Implicated in endothelial developmental
CC processes later and distinct from that of VEGF. Appears to play a
CC crucial role in mediating reciprocal interactions between the
CC endothelium and surrounding matrix and mesenchyme. Mediates blood
CC vessel maturation/stability. It may play an important role in the
CC heart early development (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: Found to be expressed throughout the ovarian
CC cycle.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF093573; AAC61872.1; -; mRNA.
CC EMBL; AF032923; AAC78245.1; -; mRNA.
CC HSSP; Q8UW8; 1JC9.
CC InterPro; IPR002181; Fibrinogen_C.
CC Pfam; PF00147; Fibrinogen_C; 1.
CC SMART; SM00186; FBG; 1.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;
KW Glycoprotein; Signal.
FT SIGNAL 1 15 Potential.
FT CHAIN 16 >481 Angiopoietin-1.
FT DOMAIN 283 >481 Fibrinogen C-terminal.
FT COILED 153 261 Potential.
FT CARBOHYD 92 92 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 122 122 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 154 154 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 243 243 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 294 294 N-linked (GLCNAC. . .) (Potential).
FT DISULFID 285 314 By similarity.
FT DISULFID 438 451 By similarity.
FT NON TER 481
SQ SEQUENCE 481 AA; 55557 MW; 8EEC9ED84FC2BB50 CRC64;

Query Match 80.7%; Score 85.5; DB 1; Length 481;
Best Local Similarity 90.0%; Pred. No. 0.00024;
Matches 18; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 LCTKEGVLKGGKREBEKPF 20

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Db      264  LCTRE-VLLKGGKREKPPF 282
RESULT 13
ID      Q6GNV4_XENLA PRELIMINARY; PRT; 504 AA.
AC      Q6GNV4;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DE      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      MGC80788 protein.
GN      Name=MGC80788;
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC      Xenopodinae; Xenopus; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Spleen;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J.J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Mazza M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RL      and mouse cDNA sequences."
RN      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Spleen;
RX      MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA      Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA      Richardson P.;
RT      "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT      Initiative."
RL      Dev. Dyn. 225:384-391 (2002).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Spleen;
RA      Klein S., Gerhard D.S.;
RL      Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC073367; AAH73367.1; -; mRNA.
DR      GO; GO:0007596; P:Blood coagulation; IEA.
DR      InterPro; IPR002181; Fibrinogen_C.
DR      Pfam; PF00147; Fibrinogen_C; 1.
DR      SMART; SM00186; FBG; 1.
DR      PROSITE; PS00514; FIBRIN_AG_C DOMAIN; 1.
SQ      SEQUENCE 504 AA; 57794 MW; FA4F7D4174A7D390 CRC64;

Query Match      71.7%; Score 76; DB 2; Length 504;
Best Local Similarity 70.0%; Pred. No. 0.007;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Cy      1  LCTKEGVLKGGKREKPPF 20
        ||:|||||:|:|||||
Db      270  LCSKEGTVKVKKEKPPF 289

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RESULT 14
ID      Q9CUL6_MOUSE PRELIMINARY; PRT; 383 AA.
AC      Q9CUL6;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE      library, clone:4930463121 product:hypothetical protein, full insert
DE      sequence. (Fragment).
GN      Name=Armc4;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Testis;
RX      MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA      Carninci P., Hayashizaki Y.;
RT      "High-efficiency full-length cDNA cloning."
RL      Meth. Enzymol. 303:19-44 (1999).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Testis;
RX      MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehii Y.,
RA      Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA      Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Wynshaw-Boris A., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection."
RL      Nature 409:685-690 (2001).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Testis;
RA      The FANTOM Consortium;
RT      the RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs."
RL      Nature 420:563-573 (2002).
RN      [4]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Testis;
RX      MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA      Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
RA      Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT      "Normalization and subtraction of cap-trapper-selected cDNAs to
RT      prepare full-length cDNA libraries for rapid discovery of new genes."
RL      Genome Res. 10:1617-1630 (2000).
RN      [5]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Testis;
RX      MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA      Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA      Konno H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,
RA      Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA      Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA      Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kiza A., Hayashizaki Y.;
RT "RIKEN Integrated sequence analysis (RISA) system-384-format
RT sequencing Pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AK015498; BAB29870.2; -; mRNA.
DR Ensembl; ENSMUSG0000004280; Mus musculus.
DR MGI; MGI:1922184; Armcd4.
KW Hypothetical protein.
FT NON TER 383
SQ SEQUENCE 383 AA; 43608 MW; AA688BA4AACB01D CRC64;

Query Match 55.7%; Score 59; DB 2; Length 383;
Best Local Similarity 68.8%; Pred. No. 2.1;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGGKREE 17
Db 262 CSTGVFLNGKTEEE 277
|:|||||:|||||
|:|||||:|||||

RESULT 15
Q4RNQ8 TETNG
ID Q4RNQ8 TETNG PRELIMINARY; PRT; 178 AA.
AC Q4RNQ8;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Chromosome 2 SCAF15010, whole genome shotgun sequence.
GN ORPNames=GSTENG0031451001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud C., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Blumont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
```

```
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01015010; CAG09974.1; -; Genomic_DNA.
DR InterPro; IPR011700; bZIP_2.
DR InterPro; IPR004827; TF_bZIP.
DR Pfam; PF07716; bZIP_2; 1.
DR PROSITE; PS00217; bZIP; 1.
DR PROSITE; PS00036; bZIP_BASIC; 1.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 178 AA; 19157 MW; 832C61408C134DCF CRC64;

Query Match 51.9%; Score 55; DB 2; Length 178;
Best Local Similarity 55.6%; Pred. No. 4.1;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGGKREEKXP 19
Db 4 CCEGVLTAGKDKTEKP 21
|:|||||:|||||
|:|||||:|||||

Search completed: May 11, 2006, 11:37:15
Job time : 237 secs
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 11:37:32 ; Search time 45 Seconds
(without alignments)
35.946 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREKPP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgm2_6/ptodata/1/iaa/5 COMB.pep:*
- 2: /cgm2_6/ptodata/1/iaa/6 COMB.pep:*
- 3: /cgm2_6/ptodata/1/iaa/H COMB.pep:*
- 4: /cgm2_6/ptodata/1/iaa/PCTUS COMB.pep:*
- 5: /cgm2_6/ptodata/1/iaa/RE COMB.pep:*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	478	2	US-08-740-223A-7
2	106	100.0	478	2	US-08-709-188-7
3	106	100.0	478	2	US-10-225-060-7
4	106	100.0	495	2	US-08-740-223A-26
5	106	100.0	495	2	US-09-709-188-26
6	106	100.0	495	2	US-10-225-060-26
7	106	100.0	497	2	US-08-740-223A-14
8	106	100.0	497	2	US-09-709-188-14
9	106	100.0	497	2	US-10-225-060-14
10	106	100.0	498	1	US-08-373-579-2
11	106	100.0	498	1	US-08-418-595-2
12	106	100.0	498	1	US-08-665-926-2
13	106	100.0	498	1	US-08-348-492-2
14	106	100.0	498	2	US-09-162-437-2
15	106	100.0	498	2	US-08-740-223A-2
16	106	100.0	498	2	US-08-740-223A-20
17	106	100.0	498	2	US-09-351-457-2
18	106	100.0	498	2	US-09-561-500-2
19	106	100.0	498	2	US-09-561-108-2
20	106	100.0	498	2	US-09-351-543-2
21	106	100.0	498	2	US-09-561-526-2
22	106	100.0	498	2	US-09-202-491-5
23	106	100.0	498	2	US-09-202-491-6
24	106	100.0	498	2	US-08-817-318-2
25	106	100.0	498	2	US-09-709-188-2
26	106	100.0	498	2	US-09-709-188-20
27	106	100.0	498	2	US-09-561-499-2

28 106 100.0 498 2 US-09-442-717-2 Sequence 2, Appli
29 106 100.0 498 2 US-09-689-020-2 Sequence 2, Appli
30 106 100.0 498 2 US-09-998-831-2 Sequence 2, Appli
31 106 100.0 498 2 US-09-561-005-2 Sequence 2, Appli
32 106 100.0 498 2 US-09-819-386-2 Sequence 2, Appli
33 106 100.0 498 2 US-09-351-598-2 Sequence 2, Appli
34 106 100.0 498 2 US-10-225-060-2 Sequence 2, Appli
35 106 100.0 498 2 US-10-225-060-20 Sequence 20, Appli
36 106 100.0 498 2 US-10-018-386-3 Sequence 3, Appli
37 106 100.0 498 2 US-10-215-224-5 Sequence 5, Appli
38 106 100.0 498 2 US-10-215-224-6 Sequence 6, Appli
39 106 100.0 498 2 US-10-214-812-5 Sequence 5, Appli
40 106 100.0 498 2 US-10-214-812-6 Sequence 6, Appli
41 106 100.0 498 2 US-09-562-245-2 Sequence 2, Appli
42 96 90.6 495 2 US-09-351-457-5 Sequence 5, Appli
43 96 90.6 495 2 US-09-561-500-5 Sequence 5, Appli
44 96 90.6 495 2 US-09-561-108-5 Sequence 5, Appli
45 96 90.6 495 2 US-09-351-543-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-740-223A-7
; Sequence 7, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; TITLE OF INVENTION: Intercellular Signalling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 60/022/999
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Covert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Mature Tll protein
; LOCATION: 1..478
; OTHER INFORMATION:
US-08-740-223A-7
Query Match 100.0%; Score 106; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREKPKF 20
Db 244 LCTKEGVLLKGGKREKPKF 263

RESULT 2
US-09-709-188-7
; Sequence 7, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-2
; CURRENT APPLICATION NUMBER: US/09/709,188
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-709-188-7

Query Match 100.0%; Score 106; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREKPKF 20
Db 244 LCTKEGVLLKGGKREKPKF 263

RESULT 3
US-10-225-060-7
; Sequence 7, Application US/10225060
; Patent No. 6825008
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-2
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-060-7

Query Match 100.0%; Score 106; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREKPKF 20
Db 244 LCTKEGVLLKGGKREKPKF 263

RESULT 4
US-08-740-223A-26
; Sequence 26, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-2
; CURRENT APPLICATION NUMBER: US/09/709,188
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
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; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 60/022/999
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: 2NIC1P (chimera 4)
; LOCATION: 1..495
; OTHER INFORMATION:
US-08-740-223A-26

Query Match 100.0%; Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREKPKF 20
Db 261 LCTKEGVLLKGGKREKPKF 280

RESULT 5
US-09-709-188-26
; Sequence 26, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-2
; CURRENT APPLICATION NUMBER: US/09/709,188
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
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; OTHER INFORMATION: 2N1C1P (chimera 4)
US-09-709-188-26
Query Match      100.0%; Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
Db 261 LCTKEGVLKGGKREBEKPF 280

RESULT 6
US-10-225-060-26
; Sequence 26, Application US/10225060
; Patent No. 6825008
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; OTHER INFORMATION: 2N1C1P (chimera 4)
US-10-225-060-26
Query Match      100.0%; Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
Db 261 LCTKEGVLKGGKREBEKPF 280

RESULT 7
US-08-740-223A-14
; Sequence 14, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed ligand - Vascular
; TITLE OF INVENTION: Intercellular Signalling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536

; OTHER INFORMATION: 2N1C1P (chimera 4)
US-09-709-188-26
Query Match      100.0%; Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
Db 261 LCTKEGVLKGGKREBEKPF 280

RESULT 8
US-09-709-188-14
; Sequence 14, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/09/709,188
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Mus sp.
; OTHER INFORMATION:
; OTHER INFORMATION: mouse TIE-2 ligand 1
US-08-740-223A-14
Query Match      100.0%; Score 106; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
Db 263 LCTKEGVLKGGKREBEKPF 282

RESULT 9
US-10-225-060-14
; Sequence 14, Application US/10225060
; Patent No. 6825008
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
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; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-225-060-14

Query Match
Best Local Similarity 100.0%; Score 106; DB 2; Length 497;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREKEKPF 20
   |||||
Db 263 LCTKEGVLLKGGKREKEKPF 282

RESULT 10
US-08-373-579-2
; Sequence 2, Application US/08373579
; Patent No. 5650490
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,579
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-373-579-2

Query Match
100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREKEKPF 20
   |||||
Db 264 LCTKEGVLLKGGKREKEKPF 283

RESULT 12
US-08-665-926-2

Query Match
100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREKEKPF 20
   |||||
Db 264 LCTKEGVLLKGGKREKEKPF 283

RESULT 11
US-08-418-595-2
; Sequence 2, Application US/08418595
; Patent No. 5814464
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,595
; FILING DATE: 06-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,579
; FILING DATE: 17-JAN-1995
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-418-595-2

Query Match
100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREKEKPF 20
   |||||
Db 264 LCTKEGVLLKGGKREKEKPF 283

RESULT 12
US-08-665-926-2
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; Sequence 2, Application US/08665926
; Patent No. 5851797
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al.
; TITLE OF INVENTION: TIE-2 LIGAND-3, METHODS OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,926
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert J. Cobert
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-2113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-665-926-2

Query Match 100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREEEKPF 20
Db 264 LCTKEGVLLKGGKREEEKPF 283

RESULT 13
US-08-348-492-2
; Sequence 2, Application US/08348492
; Patent No. 5879672
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,492
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.

; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempler, Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 330B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 347-7000
; TELEFAX: (914) 347-2113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-348-492-2

Query Match 100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREEEKPF 20
Db 264 LCTKEGVLLKGGKREEEKPF 283

RESULT 14
US-09-162-437-2
; Sequence 2, Application US/09162437
; Patent No. 6166185
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/162,437
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/418,595
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,579
; FILING DATE: 17-JAN-1995
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.

REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-162-437-2

Query Match 100.0%; Score 106; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREBEKPF 20
|||||
Db 264 LCTKEGVLLKGGKREBEKPF 283

RESULT 15
US-08-740-223A-2
Sequence 2, Application US/08740223A
Patent No. 6265564
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: Expressed Ligand - Vascular
TITLE OF INVENTION: Intercellular Signalling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Covert, Robert J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 333
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Human TIE-2 ligand 1
LOCATION: 1...498
OTHER INFORMATION: from clone gt10 encoding htie-2
OTHER INFORMATION: ligand 1
US-08-740-223A-2

Query Match 100.0%; Score 106; DB 2; Length 498;

Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGGKREBEKPF 20
|||||
Db 264 LCTKEGVLLKGGKREBEKPF 283
Search completed: May 11, 2006, 11:38:49
Job time : 46 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 11:38:12 ; Search time 166 Seconds
(without alignments)
50.341 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREBEKPF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	20	4	US-10-789-222-1
2	106	100.0	20	4	US-10-789-222-2
3	106	100.0	235	3	US-09-832-355A-18
4	106	100.0	260	4	US-10-273-180-2
5	106	100.0	298	4	US-10-273-180-4
6	106	100.0	309	4	US-10-273-180-6
7	106	100.0	312	4	US-10-273-180-8
8	106	100.0	402	4	US-10-367-259A-36
9	106	100.0	402	6	US-11-019-829-115
10	106	100.0	456	4	US-10-789-222-7
11	106	100.0	456	4	US-10-789-222-8
12	106	100.0	478	4	US-10-225-060-7
13	106	100.0	478	5	US-10-928-911-7
14	106	100.0	478	6	US-11-073-120-7
15	106	100.0	495	4	US-10-225-060-26
16	106	100.0	495	5	US-10-928-911-26
17	106	100.0	495	6	US-11-073-120-26
18	106	100.0	497	4	US-10-225-060-14
19	106	100.0	497	5	US-10-928-911-14
20	106	100.0	497	6	US-11-073-120-14
21	106	100.0	498	3	US-09-998-831-2
22	106	100.0	498	3	US-09-897-306-13
23	106	100.0	498	3	US-09-832-355A-15
24	106	100.0	498	3	US-09-998-833-2
25	106	100.0	498	4	US-10-179-744-2
26	106	100.0	498	4	US-10-186-817-2
27	106	100.0	498	4	US-10-215-224-5

28	106	100.0	498	4	US-10-215-224-6	Sequence 6, Appli
29	106	100.0	498	4	US-10-214-812-5	Sequence 5, Appli
30	106	100.0	498	4	US-10-214-812-6	Sequence 5, Appli
31	106	100.0	498	4	US-10-225-060-2	Sequence 2, Appli
32	106	100.0	498	4	US-10-225-060-20	Sequence 20, Appli
33	106	100.0	498	4	US-10-321-332-2	Sequence 2, Appli
34	106	100.0	498	4	US-10-136-819-12	Sequence 12, Appli
35	106	100.0	498	4	US-10-179-615-2	Sequence 2, Appli
36	106	100.0	498	4	US-10-179-820-2	Sequence 2, Appli
37	106	100.0	498	4	US-10-373-561-2	Sequence 2, Appli
38	106	100.0	498	4	US-10-367-259A-13	Sequence 13, Appli
39	106	100.0	498	4	US-10-367-259A-14	Sequence 14, Appli
40	106	100.0	498	4	US-10-367-259A-24	Sequence 24, Appli
41	106	100.0	498	4	US-10-367-259A-26	Sequence 26, Appli
42	106	100.0	498	4	US-10-367-259A-28	Sequence 28, Appli
43	106	100.0	498	4	US-10-367-259A-40	Sequence 40, Appli
44	106	100.0	498	4	US-10-789-222-13	Sequence 13, Appli
45	106	100.0	498	4	US-10-789-222-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1

US-10-789-222-1

; Sequence 1, Application US/10789222

; Publication No. US20040186054A1

; GENERAL INFORMATION:

; APPLICANT: Yu Qin

; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses

; TITLE OF INVENTION: of the Same

; FILE REFERENCE: UPN0003-100 (P3115)

; CURRENT APPLICATION NUMBER: US/10/789,222

; CURRENT FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: US 60/450,582

; PRIOR FILING DATE: 2003-02-27

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-789-222-1

Query Match 100.0%; Score 106; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LCTKEGVLLKGGKREBEKPF 20
|||||
Db 1 LCTKEGVLLKGGKREBEKPF 20

RESULT 2

US-10-789-222-2

; Sequence 2, Application US/10789222

; Publication No. US20040186054A1

; GENERAL INFORMATION:

; APPLICANT: Yu Qin

; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses

; TITLE OF INVENTION: of the Same

; FILE REFERENCE: UPN0003-100 (P3115)

; CURRENT APPLICATION NUMBER: US/10/789,222

; CURRENT FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: US 60/450,582

; PRIOR FILING DATE: 2003-02-27

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 20

; TYPE: PRT

; ORGANISM: mouse

US-10-789-222-2


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RESULT 8
US-10-367-259A-36
; Sequence 36, Application US/10367259A
; Publication No. US20030220250A1
; GENERAL INFORMATION:
; APPLICANT: ELLIS, LEE M.
; TITLE OF INVENTION: ANGIOPOIETIN-1 IN THE TREATMENT OF DISEASE
; FILE REFERENCE: UTSC:69BUS
; CURRENT APPLICATION NUMBER: US/10/367,259A
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,809
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-259A-36

Query Match      100.0%; Score 106; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREBEKPF 20
Db      264 LCTKEGVLLKGGKREBEKPF 283

RESULT 9
US-11-019-829-115
; Sequence 115, Application US/11019829
; Publication No. US20050136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; FILE REFERENCE: 22304
; CURRENT APPLICATION NUMBER: US/11/019,829
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: angiotensin 1 variant 2
; LOCATION: (1)..(402)
; OTHER INFORMATION: LocusID: 284; NM_139290
US-11-019-829-115

Query Match      100.0%; Score 106; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREBEKPF 20
Db      264 LCTKEGVLLKGGKREBEKPF 283

RESULT 10
US-10-789-222-7
; Sequence 7, Application US/10789222
; Publication No. US20040186054A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Qin
; TITLE OF INVENTION: Angiotensin and Fragments, Mutants, and Analogs Thereof and Uses
; FILE REFERENCE: UPN0003-100 (P3115)
; CURRENT APPLICATION NUMBER: US/10/789,222
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,582
; PRIOR FILING DATE: 2003-02-27
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; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-222-7

Query Match      100.0%; Score 106; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREBEKPF 20
Db      222 LCTKEGVLLKGGKREBEKPF 241

RESULT 11
US-10-789-222-8
; Sequence 8, Application US/10789222
; Publication No. US20040186054A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Qin
; TITLE OF INVENTION: Angiotensin and Fragments, Mutants, and Analogs Thereof and Uses
; FILE REFERENCE: UPN0003-100 (P3115)
; CURRENT APPLICATION NUMBER: US/10/789,222
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,582
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 456
; TYPE: PRT
; ORGANISM: mouse
US-10-789-222-8

Query Match      100.0%; Score 106; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREBEKPF 20
Db      222 LCTKEGVLLKGGKREBEKPF 241

RESULT 12
US-10-225-060-7
; Sequence 7, Application US/10225060
; Publication No. US20030092891A1
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-060-7

Query Match      100.0%; Score 106; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LCTKEGVLLKGGKREKPF 20
Db 244 LCTKEGVLLKGGKREKPF 263

RESULT 13
US-10-928-911-7
; Sequence 7, Application US/10928911
; Publication No. US20050106099A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; TITLE OF INVENTION: Intercellular Signaling Molecule
; FILE REFERENCE: REG 333X
; CURRENT APPLICATION NUMBER: US/10/928,911
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: 10/225,060
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-928-911-7

Query Match 100.0%; Score 106; DB 5; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREKPF 20
Db 244 LCTKEGVLLKGGKREKPF 263

RESULT 14
US-11-073-120-7
; Sequence 7, Application US/11073120
; Publication No. US2005018665A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; TITLE OF INVENTION: Intercellular Signaling Molecule
; FILE REFERENCE: REG 333X
; CURRENT APPLICATION NUMBER: US/11/073,120
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/225,060
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 09/709,188
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-073-120-7

Query Match 100.0%; Score 106; DB 6; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREKPF 20
Db 244 LCTKEGVLLKGGKREKPF 263

RESULT 15
US-10-225-060-26
; Sequence 26, Application US/10225060
; Publication No. US20030092891A1
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; TITLE OF INVENTION: Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; FEATURE:
; OTHER INFORMATION: 2N1CLF (chimera 4)
US-10-225-060-26

Query Match 100.0%; Score 106; DB 4; Length 495;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREKPF 20
Db 261 LCTKEGVLLKGGKREKPF 280

Search completed: May 11, 2006, 11:41:41
Job time : 167 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 11:39:02 ; Search time 27 Seconds
(without alignments)
34.777 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREKEKPF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.New.*
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2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
7: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
8: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
10: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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12: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	100.0	260	11	US-11-284-465-2
2	106	100.0	298	11	US-11-284-465-4
3	106	100.0	309	11	US-11-284-465-6
4	106	100.0	312	11	US-11-284-465-8
5	106	100.0	498	11	US-11-254-137-2
6	96	90.6	495	11	US-11-254-137-5
7	89.5	84.4	497	11	US-11-149-462-11
8	89.5	84.4	497	11	US-11-049-536-163
9	89.5	84.4	497	11	US-11-199-739-163
10	45	42.5	482	11	US-11-188-298-21319
11	45	42.5	923	11	US-11-075-047A-113
12	44.5	42.0	249	11	US-11-096-568A-24481
13	44.5	42.0	260	11	US-11-096-568A-24480
14	44.5	42.0	354	11	US-11-096-568A-24479
15	44	41.5	275	11	US-11-110-977-2
16	44	41.5	282	11	US-11-264-096-458
17	44	41.5	318	11	US-11-264-096-455
18	44	41.5	798	11	US-11-079-463-10034
19	43	40.6	113	8	US-10-370-959-74
20	43	40.6	415	11	US-11-182-946-6
21	43	40.6	589	9	US-10-467-657-4826

Sequence 5254, Ap
Sequence 8728, Ap
Sequence 10154, A
Sequence 2598, Ap
Sequence 18, Appli
Sequence 1, Appli
Sequence 412, App
Sequence 10907, A
Sequence 3366, Ap
Sequence 7860, Ap
Sequence 26219, A
Sequence 7966, Ap
Sequence 1558, Ap
Sequence 1557, Ap
Sequence 1559, Ap
Sequence 96, Appli
Sequence 26218, A
Sequence 585, App
Sequence 17427, A
Sequence 10250, A
Sequence 2, Appli
Sequence 1168, Ap
Sequence 40, Appli
Sequence 40, Appli

22 43 40.6 706 11 US-11-087-099-5254
23 43 40.6 708 11 US-11-087-099-8728
24 43 40.6 1060 11 US-11-079-463-10154
25 42.5 40.1 163 9 US-10-793-626-2598
26 42 39.6 140 11 US-11-177-509-18
27 42 39.6 140 11 US-11-185-907-1
28 42 39.6 243 9 US-10-506-454-412
29 42 39.6 440 11 US-11-188-298-10907
30 42 39.6 592 11 US-11-072-512-3366
31 41 38.7 134 9 US-10-467-657-7860
32 41 38.7 362 11 US-11-096-568A-26219
33 41 38.7 394 9 US-10-467-657-7966
34 41 38.7 407 11 US-11-172-740-1558
35 41 38.7 409 11 US-11-172-740-1557
36 41 38.7 409 11 US-11-172-740-1559
37 41 38.7 412 11 US-11-082-389-96
38 41 38.7 418 11 US-11-096-568A-26218
39 41 38.7 488 11 US-11-188-298-585
40 41 38.7 547 11 US-11-188-298-17427
41 40.5 38.2 176 11 US-11-079-463-10250
42 40 37.7 127 11 US-11-205-031-2
43 40 37.7 206 9 US-10-784-004-1168
44 40 37.7 257 9 US-10-632-150-40
45 40 37.7 257 10 US-11-106-014-40

ALIGNMENTS

RESULT 1
US-11-284-465-2
; Sequence 2, Application US/11284465
; Publication No. US20060074230A1
; GENERAL INFORMATION:
; APPLICANT: KOH, Gou Young
; TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
; FILE REFERENCE: 10010-00001
; CURRENT APPLICATION NUMBER: US/11/284,465
; CURRENT FILING DATE: 2005-11-21
; PRIOR APPLICATION NUMBER: US/10/273,180
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-284-465-2

Query Match 100.0%; Score 106; DB 11; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREKEKPF 20
Db 27 LCTKEGVLLKGGKREKEKPF 46

RESULT 2
US-11-284-465-4
; Sequence 4, Application US/11284465
; Publication No. US20060074230A1
; GENERAL INFORMATION:
; APPLICANT: KOH, Gou Young
; TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
; FILE REFERENCE: 10010-00001
; CURRENT APPLICATION NUMBER: US/11/284,465
; CURRENT FILING DATE: 2005-11-21
; PRIOR APPLICATION NUMBER: US/10/273,180
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

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;
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; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-284-465-4

Query Match      100.0%; Score 106; DB 11; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20
Db 64 LCTKEGVLKGGKREKEKPF 83

RESULT 3
US-11-284-465-6
; Sequence 6, Application US/11284465
; Publication No. US20060074230A1
; GENERAL INFORMATION:
; APPLICANT: KOH, Gou Young
; TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
; FILE REFERENCE: 10010-00001
; CURRENT APPLICATION NUMBER: US/11/284,465
; CURRENT FILING DATE: 2005-11-21
; PRIOR APPLICATION NUMBER: US/10/273,180
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-284-465-6

Query Match      100.0%; Score 106; DB 11; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20
Db 75 LCTKEGVLKGGKREKEKPF 94

RESULT 4
US-11-284-465-8
; Sequence 8, Application US/11284465
; Publication No. US20060074230A1
; GENERAL INFORMATION:
; APPLICANT: KOH, Gou Young
; TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
; FILE REFERENCE: 10010-00001
; CURRENT APPLICATION NUMBER: US/11/284,465
; CURRENT FILING DATE: 2005-11-21
; PRIOR APPLICATION NUMBER: US/10/273,180
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-284-465-8

Query Match      100.0%; Score 106; DB 11; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20
Db 78 LCTKEGVLKGGKREKEKPF 97

RESULT 5
US-11-254-137-2
; Sequence 2, Application US/11254137
; Publication No. US20060083745A1
; GENERAL INFORMATION:
; APPLICANT: THORPE, PHILIP E.
; APPLICANT: RAN, SOPHIA
; TITLE OF INVENTION: CANCER TREATMENT KITS COMPRISING THERAPEUTIC CONJUGATES
; TITLE OF INVENTION: THAT BIND TO AMINOPHOSPHOLIPIDS
; FILE REFERENCE: 4001.002383
; CURRENT APPLICATION NUMBER: US/11/254,137
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US/09/351,149
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-254-137-2

Query Match      100.0%; Score 106; DB 11; Length 498;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20
Db 264 LCTKEGVLKGGKREKEKPF 283

RESULT 6
US-11-254-137-5
; Sequence 5, Application US/11254137
; Publication No. US20060083745A1
; GENERAL INFORMATION:
; APPLICANT: THORPE, PHILIP E.
; APPLICANT: RAN, SOPHIA
; TITLE OF INVENTION: CANCER TREATMENT KITS COMPRISING THERAPEUTIC CONJUGATES
; TITLE OF INVENTION: THAT BIND TO AMINOPHOSPHOLIPIDS
; FILE REFERENCE: 4001.002383
; CURRENT APPLICATION NUMBER: US/11/254,137
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US/09/351,149
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-254-137-5

Query Match      90.6%; Score 96; DB 11; Length 495;
Best Local Similarity 95.0%; Pred. No. 1.8e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20
Db 261 LCTKEGVLKGGKREKEKPF 280

RESULT 7
US-11-149-462-11
; Sequence 11, Application US/11149462
; Publication No. US20060002978A1
; GENERAL INFORMATION:
; APPLICANT: Shea, Lonnie D.
; APPLICANT: Shea, Lonnie L.
; APPLICANT: Whittlesey, Kevin
; APPLICANT: Yang, Yang
; APPLICANT: Rives, Christopher
; APPLICANT: Rovedo, Mark
; APPLICANT: Iskandar, Bermans
```

; TITLE OF INVENTION: Biodegradable Scaffolds and Uses Thereof
 ; FILE REFERENCE: 1720-1-011N
 ; CURRENT APPLICATION NUMBER: US/11/149,462
 ; PRIOR FILING DATE: 2005-06-09
 ; PRIOR APPLICATION NUMBER: 60/578,785
 ; PRIOR FILING DATE: 2004-06-10
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 497
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-149-462-11

Query Match 84.4%; Score 89.5; DB 11; Length 497;
 Best Local Similarity 95.0%; Pred. No. 2e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 LCTKEGVLKGGKREKPF 20
 ||||| ||||| ||||| ||||| |||||
 Db 264 LCTKE-VLLKGGKREKPF 282

RESULT 8
 US-11-049-536-163
 ; Sequence 163, Application US/11/049536
 ; Publication No. US20060024297A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wood, Clive R.
 ; APPLICANT: Dransfield, Daniel T.
 ; APPLICANT: Pieters, Henk
 ; APPLICANT: Hoet, Rene
 ; APPLICANT: Hufton, Simon E.
 ; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
 ; FILE REFERENCE: 10280-128001
 ; CURRENT APPLICATION NUMBER: US/11/049,536
 ; CURRENT FILING DATE: 2005-02-02
 ; PRIOR APPLICATION NUMBER: US 10/916,840
 ; PRIOR FILING DATE: 2004-08-12
 ; PRIOR APPLICATION NUMBER: US 60/494,713
 ; PRIOR FILING DATE: 2003-08-12
 ; NUMBER OF SEQ ID NOS: 721
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 163
 ; LENGTH: 497
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-049-536-163

Query Match 84.4%; Score 89.5; DB 11; Length 497;
 Best Local Similarity 95.0%; Pred. No. 2e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 LCTKEGVLKGGKREKPF 20
 ||||| ||||| ||||| ||||| |||||
 Db 264 LCTKE-VLLKGGKREKPF 282

RESULT 9
 US-11-199-739-163
 ; Sequence 163, Application US/11/199739
 ; Publication No. US20060057138A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wood, Clive R.
 ; APPLICANT: Dransfield, Daniel T.
 ; APPLICANT: Pieters, Henk
 ; APPLICANT: Hoet, Rene
 ; APPLICANT: Hufton, Simon E.
 ; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
 ; FILE REFERENCE: 10280-135001
 ; CURRENT APPLICATION NUMBER: US/11/199,739
 ; CURRENT FILING DATE: 2005-08-09
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 163
 ; LENGTH: 497
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-199-739-163

; PRIOR FILING DATE: 2005-02-02
 ; PRIOR APPLICATION NUMBER: US 10/916,840
 ; PRIOR FILING DATE: 2004-08-12
 ; PRIOR APPLICATION NUMBER: US 60/494,713
 ; PRIOR FILING DATE: 2003-08-12
 ; NUMBER OF SEQ ID NOS: 726
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 163
 ; LENGTH: 497
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-199-739-163

Query Match 84.4%; Score 89.5; DB 11; Length 497;
 Best Local Similarity 95.0%; Pred. No. 2e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 LCTKEGVLKGGKREKPF 20
 ||||| ||||| ||||| ||||| |||||
 Db 264 LCTKE-VLLKGGKREKPF 282

RESULT 10
 US-11-188-298-21319
 ; Sequence 21319, Application US/11/188298
 ; Publication No. US20060075522A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(53452)B
 ; CURRENT APPLICATION NUMBER: US/11/188,298
 ; CURRENT FILING DATE: 2005-07-22
 ; PRIOR APPLICATION NUMBER: 60/592,978
 ; PRIOR FILING DATE: 2004-07-31
 ; NUMBER OF SEQ ID NOS: 22569
 ; SEQ ID NO 21319
 ; LENGTH: 482
 ; TYPE: PRT
 ; ORGANISM: Geobacillus stearothermophilus
 US-11-188-298-21319

Query Match 42.5%; Score 45; DB 11; Length 482;
 Best Local Similarity 75.0%; Pred. No. 25;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 GVLLKGGKREER 17
 ||||| ||||| :||
 Db 340 GVLLKGGKREKKE 351

RESULT 11
 US-11-075-047A-113
 ; Sequence 113, Application US/11/075047A
 ; Publication No. US20060030000A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALITALO, et al.
 ; TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
 ; FILE REFERENCE: 28967/39700A
 ; CURRENT APPLICATION NUMBER: US/11/075,047A
 ; CURRENT FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: US 60/550,907
 ; PRIOR FILING DATE: 2004-03-07
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 113
 ; LENGTH: 923
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-075-047A-113

Query Match 42.5%; Score 45; DB 11; Length 923;
 Best Local Similarity 46.7%; Pred. No. 51;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GVLLKGGKREEEKP 20
|:|||||
Db 497 GIIIQGKHRENKVF 511

RESULT 12

US-11-096-568A-24481
; Sequence 24481, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24481
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(249)
; OTHER INFORMATION: Ceres Seq. ID no. 12435351
US-11-096-568A-24481

Query Match 42.0%; Score 44.5; DB 11; Length 249;
Best Local Similarity 37.5%; Pred. No. 15;
Matches 12; Conservative 2; Mismatches 3; Indels 15; Gaps 1;

Qy 3 TKEGVLLK-----GGKREBEKP 19
|:|||||
Db 44 TEEGVLLKWRARYGSTLQSCVILGGTRVDRKP 75

RESULT 13

US-11-096-568A-24480
; Sequence 24480, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24480
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(260)
; OTHER INFORMATION: Ceres Seq. ID no. 12435350
US-11-096-568A-24480

Query Match 42.0%; Score 44.5; DB 11; Length 260;
Best Local Similarity 37.5%; Pred. No. 16;
Matches 12; Conservative 2; Mismatches 3; Indels 15; Gaps 1;

Qy 3 TKEGVLLK-----GGKREBEKP 19
|:|||||
Db 55 TEEGVLLKWRARYGSTLQSCVILGGTRVDRKP 86

RESULT 14

US-11-096-568A-24479
; Sequence 24479, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24479
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(354)
; OTHER INFORMATION: Ceres Seq. ID no. 12435349
US-11-096-568A-24479

Query Match 42.0%; Score 44.5; DB 11; Length 354;
Best Local Similarity 37.5%; Pred. No. 22;
Matches 12; Conservative 2; Mismatches 3; Indels 15; Gaps 1;

Qy 3 TKEGVLLK-----GGKREBEKP 19
|:|||||
Db 149 TEEGVLLKWRARYGSTLQSCVILGGTRVDRKP 180

RESULT 15

US-11-110-977-2
; Sequence 2, Application US/11110977
; Publication No. US20050260682A1
; GENERAL INFORMATION:
; APPLICANT: Charmley, Patrick R.
; APPLICANT: Smith, Ryan C.
; APPLICANT: Argonza-Barrett, Rhodora H.
; APPLICANT: Fitzgibbon, Matthew P.
; APPLICANT: Wang, Kai P.
; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
; FILE REFERENCE: CECH18764
; CURRENT APPLICATION NUMBER: US/11/110,977
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/112,645
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/280,514
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-110-977-2

Query Match 41.5%; Score 44; DB 11; Length 275;
Best Local Similarity 52.9%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREES 17
|:|||||
Db 254 LCSSEVLLKNAEREQE 270

Search completed: May 11, 2006, 11:42:14
Job time : 28 secs